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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:32:19 ; Search time 55 Seconds (without alignments)

164.391 Million cell updates/sec

Title: US-09-902-517-49

Perfect score: 169

Sequence: 1 SPKMQVQGSGCFGRKMDRISSSGLGCKVLRHH 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	169	100.0	32	AAR40861
2	169	100.0	32	AAR34301
3	169	100.0	32	AAR36381
4	169	100.0	32	AAW70090
5	169	100.0	32	AAW67040
6	169	100.0	32	AAB82550
7	169	100.0	32	AAB91333
8	169	100.0	32	AAB91340
9	169	100.0	32	AAB45739
10	169	100.0	32	AAE12434
11	169	100.0	32	ABG98205
12	169	100.0	32	ADA00765
13	169	100.0	32	ADA00784
14	169	100.0	32	ABU63215
15	169	100.0	32	ADD55931
16	169	100.0	32	ADD93296
17	169	100.0	33	AAR45762
18	169	100.0	33	AAR35490
19	169	100.0	34	AAR45761
20	169	100.0	34	ADD93297
21	169	100.0	108	AAB45738
22	169	100.0	109	AAB96183
23	169	100.0	118	AAR06603
24	169	100.0	134	AAR04087
25	169	100.0	134	AAY05325

ALIGNMENTS

RESULT	1
ID	AAR40861 standard; protein; 32 AA.
XX	
AC	AAR40861;
XX	
DT	14-MAR-1994 (first entry)
XX	
DE	BNP.
XX	
KW	BNP; brain natriuretic peptide; transformation; expression; cloning; puci19; protease V8.
XX	
OS	Homo sapiens.
XX	
PN	JP05207891-A.
XX	
PD	20-AUG-1993.
XX	
PF	08-MAR-1991; 91JP-00043641.
XX	
PR	08-MAR-1991; 91JP-00043641.
XX	
PA	(SHIO) SHIONOGI & CO LTD.
XX	
DR	WPI; 1993-297469/38.
XX	
N-PSDB;	AAQ47829.
PT	Brain natriuretic peptide prep. - by forming fused peptide contg. desired sequence, cleaving with restriction enzyme and collecting desired peptide.
PT	Disclosure; Page 8; 11pp; Japanese.
PT	The prepn. of BNP comprises: (a) obtaining a fused protein protein of formula X-Glu-BNP, where X is a leader sequence of 70-170 amino acids (AAR45761); (b) cleaving the fused protein with a restriction enzyme that can cleave between Glu and BNP. (c) collecting BNP. The BNP sequence is shown in (AAQ47829) and the Glu-BNP sequence is given in (AAQ47831)
PS	Sequence 32 AA;
CC	SPKMQVQGSGCFGRKMDRISSSGLGCKVLRHH 32

Query Match 100.0%; Score 169; DB 2; Length 32;

Best Local Similarity 100.0%; Pred. No. 1e-16;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPKMQVQGSGCFGRKMDRISSSGLGCKVLRHH 32

QY 2 AAY05325 Human gam

RESULT 2	23-MAR-1993.
ID AAR34301	10-SEP-1991; 91JP-00230597.
ID AAR34301 standard; protein; 32 AA.	XX
AC AAR34301;	XX
XX	XX
DT 28-JUL-1993 (first entry)	XX
DE Mutated hBNP.	XX
DE Wild type; brain natriuretic peptide; BNP; modify; Asp-Pro.	XX
OS Homo sapiens.	XX
XX	XX
PN JP05056794-A.	XX
XX	XX
PD 09-MAR-1993.	XX
PR 03-SEP-1991; 91JP-00222783.	XX
PR 03-SEP-1991; 91JP-00222783.	XX
PA (DAUC) DAIICHI KAGAKU YAKUHIN KK.	XX
PA (DAUC) DAIICHI PHARM CO LTD.	XX
PA WPI; 1993-120386/15.	XX
DR WPI; 1993-120386/15.	XX
PT Physiologically active peptide prepn. e.g. human brain natriuretic peptide - by culturing transformed cells having gene which encodes fused protein of active and protective peptide(s), collecting and cleaving PT protein.	XX
PT	XX
PS Disclosure; Page 6; 16pp; Japanese.	XX
PS	XX
CC The sequences given in AAR34301-02 are mutated brain natriuretic peptides (hBNP). These peptides have been modified such that the Asp in the N-terminal Asp-Pro linkage may be replaced by Ser or may be deleted.	CC
CC	CC
CC	CC
XX	CC
SQ Sequence 32 AA;	CC
Query Match 100.0%; Score 169; DB 2; Length 32;	CC
Best Local Similarity 100.0%; Pred. No. 1e-16; 0; Mismatches 0; Indels 0; Gaps 0;	CC
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC
Query 1 SPKMWQGSGCFGRKMDRISSSSGLGCKVLRHH 32	CC
Db 1 SPKMWQGSGCFGRKMDRISSSSGLGCKVLRHH 32	CC
Sequence 32 AA;	CC
PS	XX
RESULT 3	RESULT 4
AAR36381	AAW70090
ID AAR36381 standard; protein; 32 AA.	ID AAW70090 standard; peptide; 32 AA.
XX	XX
AC AAR36381;	AC AAW70090;
XX	XX
DT 29-JUL-1993 (first entry)	DT 28-OCT-1998 (first entry)
XX	XX
DE Brain natriuretic peptide (BNP) 1.	DE Brain natriuretic peptide (BNP) 1.
XX	XX
KW BNP; brain natriuretic peptide; cardiac disease; cardiac hypertrophy; chronic heart failure; ischaemic cardiac disease; arrhythmia; cGMP; pulmonary blood circulation; haemodynamic property.	XX
XX	XX
OS Unidentified.	OS
XX	XX
PN WO9834636-A1.	PN
XX	XX
PD 13-AUG-1998.	PD
XX	XX
PF 05-FEB-1998; 98WO-JP000483.	PF
XX	XX
PR 05-FEB-1997; 97JP-00022594.	PR
XX	XX
PA (SUNR) SUNTORY LTD.	PA
XX	XX
PI Inomata N, Yamaki A, Furuya M, Hidaka T;	PI
XX	XX
KW WPI; 1998-446949/38.	KW
XX	XX
DE Recombinant hBNP.	DE
XX	XX
KW Plasmid; fusion peptide; murine; rat; interleukin 1; IL-1; human; brain natriuretic peptide; hBNP; recombinant; BNP.	KW
XX	XX
OS Synthetic.	OS
XX	XX
Key Location/Qualifiers	Key
FT Misc-difference 1 /note= "May be absent"	FT
PN JP05068581-A.	PN

CC	capable of binding to the peptide receptor of GC-A and promoting production of cGMP. The drug composition may be used clinically to treat cardiac diseases caused by cardiac hypertrophy, including chronic heart failure, ischaemic cardiac diseases and arrhythmia. The active substance can bind to the natriuretic peptide receptor of GC-A and promote production of cGMP, effectively preventing cardiac hypertrophy and leading to improvement of the pulmonary blood circulation. The substance does not affect haemodynamic properties, blood pressure, heart beat and urine volume.	PA (NOVO) NOVO-NORDISK A.S.
CC		XX
CC		PI Huusfeldt PO, Madsen K, Knudsen LB;
CC		XX DR WPI; 1998-557474/47.
CC		XX PT Lipophilic derivatives of atrial and brain natriuretic peptides - notably as amides, prolong activity, use in hypertension, congestive heart failure, renal disorders, oedema, and hepatic cirrhosis.
CC		XX PT
CC		XX PT
CC		XX PS
CC	Sequence 32 AA;	XX Claim 32; Page 1-2; 23pp; English.
XX		XX
Query Match	100.0%; Score 169; DB 2; Length 32;	CC
Best Local Similarity	100.0%; Pred. No. 1e-16;	CC
Matchers	32; Conservative 0; Mismatches 0;	CC
QY	1 SPKQVQGSGCFGGRKMDRISSSSGLGCKVLRRH 32	CC
Db	1 SPKQVQGSGCFGGRKMDRISSSSGLGCKVLRRH 32	CC
RESULT 5		CC
ID	AAW67040	CC
XX	AAW67040 standard; peptide; 32 AA.	CC
AC	AAW67040;	CC
DT	15-DEC-1998 (first entry)	CC
XX		CC
DE	Brain natriuretic peptide (BNP).	CC
XX		CC
RW	atrial natriuretic peptide; brain natriuretic Peptide; ANP; BNP; lipophilic substituent; hypertension; congestive heart failure; oedema; renal disorder.	CC
XX		CC
OS	Mammalia.	CC
XX		CC
Key	Location/Qualifiers	CC
FR	2. .32	CC
FT	/note= "this fragment having a lipophilic group attached	CC
FT	to it is claimed in Claim 33"	CC
FT	3. .32	CC
FT	/note= "this fragment having a lipophilic group attached to it is claimed in Claim 33"	CC
FT	4. .32	CC
FT	/note= "this fragment having a lipophilic group attached to it is claimed in Claim 33"	CC
FT	5. .32	CC
FT	/note= "this fragment having a lipophilic group attached to it is claimed in Claim 33"	CC
FT	6. .32	CC
FT	/note= "this fragment having a lipophilic group attached to it is claimed in Claim 33"	CC
FT	7. .32	CC
FT	/note= "this fragment having a lipophilic group attached to it is claimed in Claim 33"	CC
FT	8. .32	CC
FT	/note= "this fragment having a lipophilic group attached to it is claimed in Claim 33"	CC
FT	9. .32	CC
FT	/note= "this fragment having a lipophilic group attached to it is claimed in Claim 33"	CC
FT	10. .26	CC
FT	/label= disulphide_bond	CC
XX		CC
PN	WO9845329-A1.	CC
XX		CC
PD	15-OCT-1998.	CC
XX		CC
PF	06-APR-1998; 98WO-DK000142.	CC
XX		CC
PR	04-APR-1997; 97US-0043400P.	CC
XX		CC
PA	(NOVO) NOVO-NORDISK A.S.	XX
XX		PI
PI	Huusfeldt PO, Madsen K, Knudsen LB;	XX
XX		DR
XX		WPI; 1998-557474/47.
XX		XX PT
XX		XX PT
XX		XX PR
XX		XX PR
XX		XX PA
XX		XX PA
XX		XX PI
XX		XX DR
XX		XX WPI; 2001-457339/49.
XX		XX XX
XX		XX PT
XX		XX PT
XX		XX PS
XX		XX Disclosure; Fig 1; 81pp; English.

CC The present sequence is that of human brain natriuretic peptide (BNP).
 CC The invention provides fusion peptides comprising a biologically active
 CC portion of *Dendroaspis natriuretic peptide* (DNP). DNP is obtained from
 CC the venom of the green mamba snake, *Dendroaspis angusticeps*. It contains
 CC a 17-amino acid disulfide ring structure similar to that of BNP. Claimed
 CC methods of treating, inhibiting or preventing heart failure in a mammal
 CC (human, rat, mouse, dog, cattle, horse, sheep, goat or cat) involve
 CC administering DNP or a chimeric peptide including a portion of DNP (see
 CC AAB82543 and AAB82544) and the N-terminal portion of especially human BNP
 CC or C-type natriuretic peptide. Such peptides may also be used to treat
 CC acute or chronic kidney failure, hypertension, cirrhosis of the liver,
 CC nephrotic syndrome and other oedematous states
 XX Sequence 32 AA;

Query Match 100.0%; Score 169; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e-16; Mismatches 0; Indels 0; Gaps 0;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPKMYQGSGCFGRKMDRISSSGLGCKVLRRH 32
 Db 1 SPKMYQGSGCFGRKMDRISSSGLGCKVLRRH 32

RESULT 7

AAB91333
 ID AAB91333 standard; peptide; 32 AA.

XX
 AC AAB91333;
 XX
 DT 22-JUN-2001 (first entry)

XX
 DE Brain natriuretic peptide (BNP) SEQ ID NO:509.
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX
 OS Homo sapiens.
 XX
 OS Synthetic.

XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.

XX
 PR 17-MAY-2000; 2000WO-US013576.

XX
 PR 17-MAY-1999; 99US-0134406P.

XX
 PR 10-SEP-1999; 99US-0153406P.

XX
 PR 15-OCT-1999; 99US-0159783P.

XX
 PA (CONJ-) CONJUCHEM INC.

XX
 PR 17-MAY-2000; 2000WO-US013576.

XX
 PR 10-SEP-1999; 99US-0153406P.

XX
 PR 15-OCT-1999; 99US-0159783P.

XX
 PA (CONJ-) CONJUCHEM INC.

XX
 PR 17-MAY-1999; 99US-0134406P.

XX
 PR 10-SEP-1999; 99US-0153406P.

XX
 PR 15-OCT-1999; 99US-0159783P.

XX
 PA (CONJ-) CONJUCHEM INC.

XX
 PR 17-MAY-2000; 2000WO-US013576.

XX
 PR 10-SEP-1999; 99US-0153406P.

XX
 PR 15-OCT-1999; 99US-0159783P.

CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX Sequence 32 AA;

Query Match 100.0%; Score 169; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e-16; Mismatches 0; Indels 0; Gaps 0;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPKMYQGSGCFGRKMDRISSSGLGCKVLRRH 32
 Db 1 SPKMYQGSGCFGRKMDRISSSGLGCKVLRRH 32

RESULT 8

AAB91340
 ID AAB91340 standard; peptide; 32 AA.

XX
 AC AAB91340;
 XX
 DT 22-JUN-2001 (first entry)

XX
 DE Brain natriuretic peptide (BNP) SEQ ID NO:516.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX
 OS Homo sapiens.
 OS Synthetic.

XX
 PN WO200069900-A2.

XX
 PD 23-NOV-2000.

XX
 PR 17-MAY-2000; 2000WO-US013576.

XX
 PR 17-MAY-1999; 99US-0134406P.

XX
 PR 10-SEP-1999; 99US-0153406P.

XX
 PR 15-OCT-1999; 99US-0159783P.

XX
 PA (CONJ-) CONJUCHEM INC.

XX
 PR Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX
 DR WPI; 2001-112059/12.

XX
 PT Modifying and attaching therapeutic peptides to albumin prevents or
 PT reduces the action of peptidases to increase length of activity (half
 PT life) and specificity as bonding to large molecules decreases

XX
 PS Disclosure; Page 369; 733pp; English.

XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX	SQ	Sequence 32 AA;	Query Match	100.0%; Score 169; DB 4; Length 32;	Score 169; DB 4; Length 32;
			Best Local Similarity	100.0%; Pred. No. 1e-16;	Best Local Similarity 100.0%; Pred. No. 1e-16;
			Matches 32; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32	QY	1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32	QY 1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32
Db	1	SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32	Db	1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32	Db 1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32
			RESULT 9		RESULT 10
			AAB45739		AAE12434
			AAB45739 standard; protein; 32 AA.		ID AAE12434 standard; peptide; 32 AA.
XX			XX		XX
AC			AC		AC AAE12434;
XX			XX		XX AAE12434;
DT			15-MAR-2001 (first entry)		03-JAN-2002 (first entry)
XX			XX		XX
DE			Human mature BNP.		Human brain natriuretic peptide (BNP).
XX			XX		XX
KW			BNP; brain natriuretic peptide; heart failure; vascular restenosis; DNP; D-type natriuretic peptide; antiarteriosclerotic; cardiant; vasoconstrictive; cardiac muscle; pulmonary hypertension; human; ss.		Prophylaxis; ischaemic heart disease; myocardial infarction; human; ischaemia reperfusion injury; ischaemic heart disease; infarct region; vasoconstrictive; brain natriuretic peptide; BNP.
KW			XX		XX
OS			OS Homo sapiens.		OS Homo sapiens.
XX			XX		XX
PN			PN WO200071576-A2.		PN
XX			XX		XX
PD			PD 30-NOV-2000.		PD 03-JAN-2002.
XX			XX		XX
PF			PF 24-MAY-2000; 2000WO-US014351.		PF 24-MAY-1999; 99US-0135490P.
XX			XX		XX
PR			PR (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.		PR (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX			XX		XX
PA			PA (SIMA/) SIMARI R.		PA (KITA/) KITAKAZE M.
XX			XX		XX
PT			PT Simari R;		PT Kitakaze M;
XX			XX		XX
DR			DR WPI; 2001-025135/03.		DR WPI; 2001-638528/73.
XX			XX		XX
PT			PT Inhibiting or preventing heart failure, hypertension and atherosclerosis, involves administering a composition comprising a nucleic acid molecule encoding brain natriuretic peptide in a delivery vehicle.		PT Composition for the treatment or prophylaxis of ischemic heart disease i.e. myocardial infarction, comprises a substance which can increase intracellular cGMP production by acting on a natriuretic peptide receptor.
PT			PT Disclosure; Page 80; 83pp; English.		PT Disclosure; Page 4; 9pp; English.
XX			XX		XX
CC			CC This invention describes a novel method for inhibiting or preventing heart failure in a mammal, by administering a composition containing a nucleic acid molecule (NAM) comprising a nucleic acid segment encoding brain natriuretic peptide (BNP), D-type natriuretic peptide (DNP) or its chimera, in a delivery vehicle. The invention also describes (1) an isolated and purified NAM (II) comprising a nucleic acid segment encoding a chimeric natriuretic peptide containing at least a portion of DNP; (2) an adeno-associated virus vector (III) comprising a NAM containing a nucleic acid segment encoding BNP, DNP or its chimera operably linked to transcriptional regulatory elements; (3) an adenovirus vector (IV) comprising a NAM containing a nucleic acid segment encoding DNP or its chimera operably linked to transcriptional regulatory elements; and (4) a composition comprising (II), (III), or (IV) and a delivery vehicle. The products of the invention have antiarteriosclerotic, cardiant and antihypertensive activity. The method is useful for inhibiting or preventing heart failure in a mammal and also to relax cardiac muscle, to increase BNP levels in a mammal, to detect progression of heart failure in a mammal subjected to brain natriuretic gene therapy, to inhibit or prevent vasospasm and pulmonary hypertension in a mammal. DNP and BNP are also useful for inhibiting or preventing atherosclerosis and vascular restenosis.		CC The invention relates to a pharmaceutical composition for the treatment or prophylaxis of ischaemic heart disease, comprises a substance as an active ingredient, which can increase intracellular cGMP production by acting on a natriuretic peptide receptor and which has an effect of reducing an infarct region. The composition is useful for suppressing ischaemia reperfusion injury in the treatment of ischaemic heart disease, preferably myocardial infarction. The present sequence is human brain natriuretic peptide (BNP)
CC			CC Sequence 32 AA;		CC Sequence 32 AA;
CC			CC Query Match 100.0%; Score 169; DB 4; Length 32;		CC Query Match 100.0%; Score 169; DB 4; Length 32;
CC			CC Best Local Similarity 100.0%; Pred. No. 1e-16;		CC Best Local Similarity 100.0%; Pred. No. 1e-16;
CC			CC Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		CC Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32	QY 1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32		QY 1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32
Db	1	SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32	Db 1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32		Db 1 SPKMQVQGSGCFCGRKMDRISSSGLGCKVLRHH 32
			RESULT 11		RESULT 11
			ID ABG98205		ID ABG98205
			ABG98205 standard; peptide; 32 AA.		ABG98205 standard; peptide; 32 AA.
SQ		Sequence 32 AA;			

Db	1 SPKMWQGSGCFGRKMDRISSSGLGCKVLRHH 32
AC	ABG98205;
XX	
DT	08-JAN-2003 (first entry)
XX	Human brain natriuretic peptide (BNP-32).
DE	
XX	
KW	Human; natriuretic peptide; NP; endochondral ossification; bone formation; cartilage; bone; signalling pathway; FGF; fibroblast growth factor; cardiovascular homeostasis; diuresis; natriuresis; vasodilation; atrial natriuretic peptide; ANP; brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP; dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B; guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP; skeletal dysplasia; achondroplasia; osteopathic.
XX	
OS	Homo sapiens.
XX	
PN	WO200274234-A2.
XX	
PD	26-SEP-2002.
XX	
PF	20-MAR-2002; 2002WO-IL000229.
XX	
PR	20-MAR-2001; 2001IL-00142118.
XX	
PR	20-MAR-2001; 2001US-0276939P.
XX	
PA	(PROC-) PROCHON BIOTECH LTD.
XX	
PI	PALEMBANG M, YAYON A;
XX	
DR	WPI; 2002-750515/81.
XX	
PT	Pharmaceutical composition useful in the treatment of skeletal dysplasias e.g. achondroplasia comprises at least one natriuretic peptide.
XX	
PS	Claim 4; Fig 3; 41pp; English.
XX	
CC	The invention discloses a pharmaceutical composition comprising at least one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC	Endochondral ossification is a fundamental mechanism for bone formation, whereby cartilage is replaced by bone. Endochondral ossification is the result of the concerted action of several signalling pathways, most notably the pathway triggered by the activation of the fibroblast growth factor (FGF). Natriuretic peptides are also known for their role in cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis peptide (DNP). NP's effect their biological role through two receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains which are activated upon ligand binding and lead to accumulation of intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and inhibition of the NEPs increases the concentration of the NPs in the circulation. The invention discloses compositions comprising NP secreting cells and methods for treating skeletal dysplasias involving transplanting or implanting the natriuretic peptide secreting cells. The NP secreting cells are useful in the manufacture of a medicament for the treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of abnormal bone and for increasing the size of bone growth plate in abnormal bone (e.g. limb bone). The compositions induce bone elongation in abnormal bone growth and enhance NP stabilisation in circulation. The sequences presented in ABG98202-ABG98272 are the CNP peptide and variants, with differing levels of activity, designed from it. The degenerate peptide is presented in ABG98206
CC	XX
SQ	Sequence 32 AA;
Query	100.0%; Score 169; DB 5; Length 32;
Match	Best Local Similarity 100.0%; pred. No. 1e-16; Matches 32; Conservative 0; Mismatches 0; Index 0; Gaps 0;
Qy	QGSGCFGRKMDRISSSGLGCKVLRHH 32

XX SQ Sequence 32 AA;
 Query Match 100.0%; Score 169; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e-16;
 Matches 32; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 QY 1 SPKMVQGSGCFGRKMDRISSSGLGCKVLRRH 32
 Db 1 SPKMVQGSGCFGRKMDRISSSGLGCKVLRRH 32

XX SQ Sequence 32 AA;
 Query Match 100.0%; Score 169; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e-16;
 Matches 32; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 QY 1 SPKMVQGSGCFGRKMDRISSSGLGCKVLRRH 32
 Db 1 SPKMVQGSGCFGRKMDRISSSGLGCKVLRRH 32

CC the treatment of various pathological conditions associated with water or
 CC electrolyte imbalance and hypertension, especially renovascular
 CC hypertension, congestive heart failure (CHF), nephrotic syndrome and
 CC hepatic cirrhosis, pulmonary disease and renal failure due to ineffective
 CC renal perfusion or reduced glomerular filtration rate, to modulate the
 CC activity of other diuretic, natriuretic or vasorelaxant compounds by
 CC binding to alternate receptors, stimulating receptor turnover, or
 CC providing alternate substrates for degradative enzyme of receptor
 CC activity and inhibiting these enzymes or receptors. The present sequence
 CC is the an ANP variant/variant of the invention.

RESULT 13
 ADA00784
 ID ADA00784 standard; peptide; 32 AA.
 XX AC ADA00784;
 XX DT 06-NOV-2003 (first entry)
 DE Human natriuretic peptide BNP 1-28.
 XX KW Human; natriuretic protein; atrial natriuretic peptide; ANP; ANP;
 KW hypotensive; hepatotropic; nephrotropic; cardiant; vasodilator;
 KW hepatotropic; respiratory; clearance receptor;
 KW natriuretic peptide receptor; hNPR-C; hANP(1-28); human A receptor;
 KW HNPR-A; neutral endopeptidase 11.24; NEP; natriuresis; diuresis;
 KW vasodilation; renal endopeptidase 11.24; aldosterone; electrolyte imbalance;
 KW hypertension; renovascular hypertension; congestive heart failure; CHF;
 KW nephrotic syndrome; hepatic cirrhosis; pulmonary disease; renal failure;
 KW mutant; mutein.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN US6525022-B1.
 XX PD 25-FEB-2003.
 XX PP 16-SEP-1998; 98US-00154390.
 XX PR 12-NOV-1993; 93US-00152994.
 PR 04-NOV-1994; 94WO-US012591.
 PR 06-JAN-1995; 95US-00362552.
 PR 11-APR-1995; 95US-00419877.
 PR 06-JUN-1995; 95US-00470846.
 XX PA (GETH) GENENTECH INC.
 XX PI Lowe DG, Cunningham BC, Oare D, McDowell RS, Burnier JP;
 DR WPI; 2003-553629/52.
 XX PT Novel variant of atrial natriuretic factor, useful as therapeutic agent
 PT for treating hypertension, congestive heart failure, nephrotic syndrome,
 PT hepatic cirrhosis, pulmonary disease and renal failure.
 XX Disclosure; Col 7; 51pp; English.

XX The invention relates to an atrial natriuretic factor (ANF, also known as
 CC ANP, a natriuretic peptide) comprising one or more amino acid
 CC substitutions selected from Gly9Thr, Gly9a, Gly9Arg, Arg11Ser, Arg11Asp,
 CC Gly16Arg, Gly16Lys, Gly16Orn, Gly16HAsp, and Gly16p-amidinophenyl Ala.
 CC Also included is a composition comprising nucleic acid encoding the ANF
 CC variant. The ANF has a decreased binding affinity for the human clearance
 CC receptor, natriuretic peptide receptor (hNPR)-C, compared to wild-type
 CC hANF(1-28) and an equal or higher binding affinity for the human A
 CC receptor, hNPR-A, compared to wild-type hANF(1-28). The binding affinity
 CC for hNPR-C is less than 50% or 10% of the affinity of wild-type ANF. The
 CC ANF variant has an increased half-life relative to wild-type hANF(1-28)
 CC when incubated with neutral endopeptidase 11.24 (NEP). The ANF variant is
 CC useful for inducing natriuresis, diuresis or vasodilation or inhibit
 CC renin-angiotensin II and aldosterone release and as therapeutic agents in

RESULT 14
 ABU63215
 ID ABU63215 standard; peptide; 32 AA.
 XX AC ABU63215;
 XX DT 15-OCT-2003 (first entry)
 DE Human brain natriuretic peptide (BNP).
 XX KW Natriuretic; renin-suppressing; diuretic; vasodilator; heart failure;
 KW cardiovascular disorder; congestive heart failure; hypertension;
 KW acute kidney failure; chronic kidney failure; liver cirrhosis;
 KW nephrotic syndrome; oedematous state; cardiant; BNP; human;
 KW brain natriuretic peptide.
 XX OS Homo sapiens.
 XX PN US2003069186-A1.
 XX PR 10-APR-2003.
 XX PF 26-MAR-2002; 2002US-00106806.
 XX PR 17-DEC-1999; 99US-00466268.
 XX PA (BURN/) BURNETT J C.
 PA (LISY/) LISY O.
 XX PI Burnett JC, Lisy O;
 DR WPI; 2003-576433/54.

XX PT Novel peptide compound useful for treating or preventing cardiovascular
 PT disorders e.g. congestive heart failure, has natriuretic, renin-
 PT suppressing, diuretic and/or vasodilator activity in mammals.
 XX Disclosure; Fig 1; 43pp; English.

XX The present invention relates to chimeric peptides having natriuretic,
 CC renin-suppressing, diuretic and/or vasodilator activity in mammals. The
 CC peptides of the invention are useful for treating heart failure in a
 CC mammal e.g. human, rat, mouse, canine, bovine, equine, ovine, caprine or
 CC feline. They are useful for treating and preventing cardiovascular
 CC disorders e.g. congestive heart failure, acute or chronic kidney failure,
 CC hypertension, cirrhosis of liver, nephrotic syndrome and other oedematous
 CC states. The present sequence represents human brain natriuretic peptide
 CC (BNP).
 XX SQ Sequence 32 AA;

Query Match 100.0%; Score 169; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPKMWQGSGCFGRKMDRISSSSGLGCKVLRH 32
 Db 1 SPKMWQGSGCFGRKMDRISSSSGLGCKVLRH 32

RESULT 15
 ADD55931
 ID ADD55931 standard; peptide; 32 AA.
 XX
 AC ADD55931;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human B-type natriuretic peptide (BNP).
 XX
 KW human; congestive heart failure; CHF; natriuretic peptide;
 B-type natriuretic peptide; BNP.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 10. .26
 XX
 PN WC2003079979-A2.
 XX
 PD 02-OCT-2003.
 XX
 PR 18-MAR-2003; 2003WO-US008215.
 XX
 PR 18-MAR-2002; 2002US-0364736P.
 XX
 PA (SCIO-) SCIOS INC.
 XX
 PI Schreiner GF;
 XX
 DR WPI; 2003-767771/72.
 XX
 PT Treating congestive heart failure (CHF) in a mammal, comprises
 PT administration of a natriuretic peptide.
 XX
 PS Disclosure; SEQ ID NO 1; 58pp; English.
 XX
 CC The invention comprises a method for treating congestive heart failure
 (CHF), the method involves administering a natriuretic peptide (e.g.
 CC human B-type natriuretic peptide). The method is useful for treating
 CC congestive heart failure in a mammal that is in a compensated or
 CC decompensated state of congestive heart failure. The present amino acid
 CC sequence represents the human B-type natriuretic peptide (BNP).
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 169; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPKMWQGSGCFGRKMDRISSSSGLGCKVLRH 32
 Db 1 SPKMWQGSGCFGRKMDRISSSSGLGCKVLRH 32

Search completed: March 29, 2004, 14:41:27
 Job time : 56 secs

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6					
OM protein - protein search, using sw model						
Run on:	March 29, 2004, 14:37:49 ; Search time 21 Seconds (without alignments)					
Title:	US-09-902-517-49					
Perfect score:	169					
Sequence:	1 SPKMQQGSGCFGRKMDRISSSGLGCKVLRHH 32					
Scoring table:	BLOSUM62					
Searched:	Gapop 10.0 , Gapext 0.5					
Total number of hits satisfying chosen parameters:	283366					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100%					
Database :	PIR_78:*					
	1: pir1:*					
	2: pir2:*					
	3: pir3:*					
	4: pir4:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score					
	Query					
	Match Length					
	DB ID					
	Description					
1	169	100.0	134	1	AWHUB	natriuretic peptide B precursor [validated] - human
2	124	73.4	103	2	A41403	N;Alternate names: brain natriuretic factor-32 (BNF-32); brain natriuretic protein pre
3	123	72.8	105	2	B36736	C;Species: Homo sapiens (man)
4	122	72.2	131	2	A33873	C;Date: 07-Sep-1990 #sequence revision 02-Dec-1994 #text_change 08-Dec-2000
5	106	62.7	131	2	A31676	C;Accession: A36736; A30163; A34143; A34661; B34661
6	101	59.8	140	1	JC1081	R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewick
7	87	51.5	149	1	AWDG	Biochem. Biophys. Res. Commun. 165, 650-658, 1989
8	87	51.5	150	1	S13107	A;Title: Human and canine gene homologs of porcine brain natriuretic peptide.
9	87	51.5	151	1	AWHUT	A;Reference number: A36736; MUID:90088474; PMID:2597152
10	87	51.5	152	1	AWBO	A;Accession: A36736
11	87	51.5	153	2	S14320	A;Molecule type: DNA
12	86	50.9	38	2	S1473	A;Residues: 1-134 <SEI>
13	83	49.1	153	1	AWRB	A;Cross-references: GB:M31776; NID:9179514; PIDN:AAA35603.1; PID:9179515
14	82	48.5	121	1	A30162	R;Sudoh, T.; Maekawa, K.; Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
15	82	48.5	152	1	AWRT	A;Title: Cloning and sequence analysis of cDNA encoding a precursor for human brain n
16	82	48.5	152	1	AWMS	A;Reference number: A30163; MUID:89193743; PMID:2522777
17	82	48.5	161	4	155480	A;Accession: A30163
18	82	48.5	161	4	155480	A;Molecule type: mRNA
19	81	47.9	128	2	S14872	A;Residues: 1-134 <SEI>
20	79	46.7	126	1	AWHUC	A;Cross-references: GB:M31776; NID:9179514; PIDN:AAA35603.1; PID:9179515
21	79	46.7	126	1	A36155	R;Hino, J.; Tateyama, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
22	79	46.7	126	2	S12988	Biochem. Biophys. Res. Commun. 167, 693-700, 1990
23	79	46.7	126	2	A55688	A;Title: Isolation and identification of human brain natriuretic peptide in hu
24	78	46.2	22	2	A35418	A;Reference number: A90161; MUID:90211249; PMID:2138890
25	77	45.6	36	2	S15821	A;Accession: A34661
26	77	45.6	121	2	A49144	A;Molecule type: protein
27	77	45.6	121	2	I49548	A;Residues: 27-58 <HN>
28	76	45.0	118	2	B54119	A;Accession: B34661
29	75	44.4	115	1	S15822	A;Molecule type: protein
ALIGNMENTS						
30	74	43.8	22	2	A36399	C-type natriuretic
31	74	43.8	27	2	A33431	atrial natriuretic
32	74	43.8	129	1	A54119	c-type natriuretic
33	72	42.6	22	2	JT0581	natriuretic peptide
34	72	42.6	30	2	S01657	atrial natriuretic
35	72	42.6	145	1	JQ0947	atrial natriuretic
36	70	41.4	135	1	A61244	natriuretic peptide
37	69	40.8	38	2	A42974	polyribonucleotide
38	54	32.0	718	2	AD2355	conserved hypothetical
39	52	30.8	111	2	AB2842	hypothetical protein
40	52	30.8	111	2	C97619	polypeptide - silk
41	52	30.8	1067	2	T18196	probable glyoxylat
42	51	30.2	594	2	T34855	yahR protein - Esc
43	50	29.6	148	2	D64760	polyribonucleotide
44	50	29.6	718	2	S74509	cartilage glycopro
45	49	29.0	383	2	A49562	

Query Match 100.0%; Score 169; DB 1; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9e-17; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRH 32
 Db 103 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRH 134

RESULT 2

aldosterone secretion inhibitory factor precursor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Mar-1995
 R;Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; De Lean, A.; Ong, H.
 Mol. Endocrinol. 3, 1823-1829, 1989
 A;Title: Purification and primary structure of pro-aldosterone secretion inhibitory fact
 A;Reference number: A41403; MUID:90114187; PMID:2532709
 A;Accession: A41403
 A;Molecule type: protein
 A;Residues: 1-131 <POR>
 R;Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; Ong, H.; de Lean, A.
 Endocrinology 124, 1591-1593, 1989
 A;Title: Aldosterone secretion inhibitory factor: a novel neuropeptide in bovine chromat
 A;Accession: A30976
 A;Molecule type: protein
 A;Residues: 69-103 <NG2>
 C;Superfamily: natriuretic peptide A precursor

Query Match 73.4%; Score 124; DB 2; Length 103;
 Best Local Similarity 71.0%; Pred. No. 1.8e-10; 0; Mismatches 4; Indels 0; Gaps 0;
 Matches 22; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 PKMVQGSGCFGRKMDRISSSGGLGCKVLRRH 32
 Db 73 PKMRDSCGCFGRRLDRIGSLSGLGCNVLRRY 103

RESULT 3

brain natriuretic peptide - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Dec-1994
 C;Accession: B36736
 R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki,
 Biochem. Biophys. Res. Commun. 165, 650-658, 1989
 A;Title: Human and canine gene homologs of porcine brain natriuretic peptide.
 A;Reference number: A36736; MUID:90088474; PMID:2597152
 A;Accession: B36736
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-105 <SEI>
 A;Cross-references: GB:M31777
 C;Superfamily: natriuretic peptide A precursor

Query Match 72.8%; Score 123; DB 2; Length 105;
 Best Local Similarity 68.8%; Pred. No. 2.5e-10; 0; Mismatches 5; Indels 0; Gaps 0;
 Matches 22; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRH 32
 Db 74 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRY 105

RESULT 4

brain natriuretic peptide precursor - pig
 C;Species: Sus scrofa domesticus (domestic pig)
 C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 16-Jul-1999
 C;Accession: A33873
 C;Accession: A33873; MUID:89214071; PMID:2708334
 R;Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 157, 402-409, 1988
 A;Title: Isolation and identification of a high molecular weight brain natriuretic peptide
 A;Reference number: A31675; MUID:89061743; PMID:3196347
 A;Accession: A31675
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 26-131 <MIN>
 C;Superfamily: natriuretic peptide A precursor

Query Match 72.2%; Score 122; DB 2; Length 131;
 Best Local Similarity 68.8%; Pred. No. 4.4e-10; 0; Mismatches 5; Indels 0; Gaps 0;
 Matches 22; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRH 32
 Db 100 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRY 131

R;Porter, J.G.; Arfsten, A.; Palisi, T.; Scarborough, R.M.; Lewicki, J.A.; Seilhamer,
 J. Biol. Chem. 264, 6689-6692, 1989
 A;Title: Cloning of a cDNA encoding porcine brain natriuretic peptide.
 A;Reference number: A33873; MUID:89214071; PMID:2708334
 A;Accession: A33873
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-131 <POR>
 A;Cross-references: GB:M25547; GB:J04708; GB:M22477; GB:M22478; NID:9164392; PIDN:AAA:
 R;Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 157, 402-409, 1988
 A;Title: Isolation and identification of a high molecular weight brain natriuretic peptide
 A;Reference number: A31675; MUID:89061743; PMID:3196347
 A;Accession: A31675
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 26-131 <MIN>
 C;Superfamily: natriuretic peptide A precursor

Query Match 72.2%; Score 122; DB 2; Length 131;
 Best Local Similarity 68.8%; Pred. No. 4.4e-10; 0; Mismatches 5; Indels 0; Gaps 0;
 Matches 22; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRH 32
 Db 100 SPKMVQGSGCFGRKMDRISSSGGLGCKVLRRY 131

A;Cross-references: GB:X01470; NID:928687; PIDN:CAA25699.1; PID:g825625
 A;Accession: B22693
 A;Molecule type: DNA
 A;Residues: 1-151,'RR' <NE2>
 A;Note: allelic variant with UGA termination codon replaced by CGA arginine codon
 R;Oikawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.; Nakazato, H.; Kangawa, K.; Fu
 Nature 309, 724-726, 1984
 A;Title: Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic factor
 A;Reference number: A001424; MUID:84219799; PMID:6203042
 A;Accession: A01424
 A;Molecule type: mRNA
 A;Residues: 1-151 <OIK>
 A;Cross-references: GB:K02043; NID:g178629; PIDN:AAE59379.1; PID:g178630
 R;Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.
 Science 226, 1206-1209, 1984
 A;Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.
 A;Reference number: A22370; MUID:85065766; PMID:6542248
 A;Accession: B29370
 A;Molecule type: DNA
 A;Residues: 1-64,'D',66-151 <SEI>
 A;Cross-references: GB:K02043
 R;Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 118, 131-139, 1984
 A;Title: Purification and complete amino acid sequence of alpha-human atrial natriuretic factor
 A;Reference number: A32733; MUID:84128019; PMID:6230082
 A;Accession: A32733
 A;Molecule type: protein
 A;Residues: 124-151 <KAN>
 R;Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S.
 Nature 310, 699-701, 1984
 A;Title: mRNA sequence for human cardiodilatin-atrial natriuretic factor precursor and
 A;Reference number: 158054; MUID:84295577; PMID:6547996
 A;Accession: 158054
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-151 <RES>
 A;Cross-references: GB:M30262; NID:g180181; PIDN:AAA35669.1; PID:g180182
 R;Vanneste, Y.; Michel, A.; Deschondt-Lanckman, M.
 Eur. J. Biochem. 196, 281-286, 1991
 A;Title: Hydrolysis of intact and Cys-Phe-cleaved human atrial natriuretic peptide in vitro
 A;Reference number: S14097; MUID:91176998; PMID:1826098
 A;Accession: S14097
 A;Molecule type: protein
 A;Residues: 124-151 <VAN>
 A;Note: natural and synthetic peptide subjected to kallikrein proteolysis
 R;Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.; Chretien, M.; Nemer, M.; Chamber
 Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984
 A;Title: Molecular cloning and characterization of DNA sequences encoding rat and human
 A;Reference number: I39458; MUID:85038509; PMID:6238331
 A;Accession: I39458
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 119-151,'RR' <RE2>
 A;Cross-references: GB:K02044; NID:9178631; PIDN:AAA51730.1; PID:g178632
 R;Maki, M.; Parmentier, M.; Inagami, T.
 Biochem. Biophys. Res. Commun. 125, 797-802, 1984
 A;Title: Cloning of genomic DNA for human atrial natriuretic factor.
 A;Reference number: I39459; MUID:8506983; PMID:6097248
 A;Accession: I39459
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-75 <RE3>
 A;Cross-references: GB:K02399; NID:g178633; PIDN:AAA35528.1; PID:g178634
 R;Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.; Homcy, C.J.; Duby, A.D.;
 Hypertension 7, 31-34, 1985
 A;Title: Molecular studies of the atrial natriuretic factor gene.
 A;Reference number: I39460
 A;Accession: I39460
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-64,'D',66-151 <RE4>
 A;Cross-references: GB:M54951; NID:g178636; PIDN:AAA35529.1; PID:g178638
 R;Greenberg, B.D.; Bencen, G.H.; Seilhamer, J.J.; Lewicki, J.A.; Fiddes, J.C.
 Nature 312, 656-658, 1984
 A;Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor precursor
 A;Reference number: I37167; MUID:85061627; PMID:6095119
 A;Accession: I37167
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 26-151 <RE5>
 A;Cross-references: EMBL:X01471; NID:g28690; PIDN:CAA25700.1; PID:g1340150
 C;Comment: Cardiodilantin is a vasoconstrictor but not a diuretic or natriuretic.
 C;Genetics:
 A;Gene: GDB:NPPA; ANP; PND
 A;Cross-references: GDB:118727; OMIM:108780
 A;Map position: 1p36-1p36
 A;Introns: 41/3; 150/3
 C;Superfamily: natriuretic peptide A precursor
 C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-151/Product: cardiodilantin #status predicted <CDD>
 F;124-151/Product: atrial alpha natriuretic peptide #status experimental <ANP>
 F;130-146/Disulfide bonds: #status experimental
 Query Match 51.5%; Score 87; DB 1; Length 151;
 Best Local Similarity 50.0%; Pred. No. 4.9e-05;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 C;Query 1 SPKMQVQGSGCFGRKMDRISSSGLGCKVLR 30
 Db 121 APRSLRRSSCFCGMRDRAQSGLGCNSFR 150
 RESULT 11
 AWBO
 atrial natriuretic peptide precursor - bovine
 N;Alternate names: ANP; atrial natriuretic polypeptide
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 18-Jun-1999
 C;Accession: A90124; A93049; A24247; A26090
 R;Vlasuk, G.P.; Miller, J.; Bencen, G.H.; Lewicki, J.A.
 Biochem. Biophys. Res. Commun. 136, 396-403, 1986
 A;Title: Structure and analysis of the bovine atrial natriuretic peptide precursor gene
 A;Reference number: A90124; MUID:86215205; PMID:2939830
 A;Accession: A90124
 A;Molecule type: DNA
 A;Residues: 1-152 <VLA>
 A;Cross-references: GB:M13145; NID:g162665; PIDN:AAA30375.1; PID:g162666
 R;Ong, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien, M.; De Lean, A.
 Life Sci. 38, 1309-1315, 1986
 A;Title: Purification and sequence determination of bovine atrial natriuretic factor.
 A;Reference number: A93049; MUID:86173941; PMID:3007908
 A;Accession: A93049
 A;Molecule type: Protein
 A;Residues: 123-150 <ONG>
 C;Genetics:
 A;Introns: 40/3; 149/3
 C;Superfamily: natriuretic peptide A precursor
 C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-152/Product: gamma atrial natriuretic factor #status predicted <ANF>
 F;123-150/Product: alpha atrial natriuretic peptide #status experimental <ANP>
 F;129-145/Disulfide bonds: #status predicted
 Query Match 51.5%; Score 87; DB 1; Length 152;
 Best Local Similarity 50.0%; Pred. No. 4.9e-05;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 C;Query 1 SPKMQVQGSGCFGRKMDRISSSGLGCKVLR 30
 Db 120 APRSLRRSSCFCGMRDRAQSGLGCNSFR 149
 RESULT 12
 S14873 atrial natriuretic peptide precursor - horse

C;Species: Equus caballus (domestic horse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
 C;Accession: S14873
 R;Maegert, H.J.; Hanke, M.; Schmeding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann, A;Submitted to the EMBL Data Library, March 1991
 A;Reference number: S14872
 A;Accession: S14873
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-153 <MAE>
 A;Cross-references: EMBL:X58563; NID:91008; PIDN:CAA41443.1; PID:g1009
 C;Superfamily: natriuretic peptide A precursor

Query Match 51.5%; Score 87; DB 2; Length 153;
 Best Local Similarity 50.0%; Pred. No. 4.9e-05; 6; Mismatches 9; Indels 0; Gaps 0;
 Matches 15; Conservative 15;

Qy 1 SPKMWQGSGCFGRKMDRISSSGIGCKVLR 30
 Db 121 APRSLRRSSCFCGGRIDRIGAQSGLGCNSFR 150

RESULT 13
 S71381
 lebetin 2 isoform alpha - Vipera lebetina
 C;Species: Vipera lebetina
 C;Accession: S71381; S71382; S71379
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-Dec-2000
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: A30162; A35691; A54893; A32918; A32919; A33253; A60735; 157704; A33252
 R;Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Kriji, M.; Fenouillet, E.; Rochat, H.; El
 FEBS Lett. 392, 6-10, 1996
 A;Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isolat
 A;Reference number: S71379; MUID:96354866; PMID:8769304
 A;Accession: S71381
 A;Molecule type: protein
 A;Residues: 1-38 <BAR>
 A;Experimental source: venom
 A;Accession: S71382
 A;Molecule type: protein
 A;Residues: 2-38 <BA2>
 A;Experimental source: venom
 A;Accession: S71379
 A;Molecule type: protein
 A;Residues: 1-13 <BA3>
 A;Experimental source: venom
 C;Keywords: anticoagulant; venom
 F;14-30/Disulfide bonds: #status predicted

Query Match 50.9%; Score 86; DB 2; Length 38;
 Best Local Similarity 64.0%; Pred. No. 1.8e-05; 7; Mismatches 7; Indels 0; Gaps 0;
 Matches 16; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 PRKMQGSGCFGRKMDRISSSGIGLC 26
 Db 6 PKKGPPNGCFGHKIDRIGSHSGLGC 30

RESULT 14
 AWRB
 atrial natriuretic peptide precursor - rabbit
 N;Alternate names: ANP; atrial natriuretic polypeptide
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
 C;Accession: B25302
 R;Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 132, 892-899, 1985
 A;Title: Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduc
 A;Reference number: A90119; MUID:86076957; PMID:2934062
 A;Accession: B25302
 A;Molecule type: mRNA
 A;Residues: 1-153 <OIK>
 A;Cross-references: GB:U02972; NID:9458021; PIDN:AAA21648.1; PID:g458022
 C;Superfamily: natriuretic peptide A precursor

Query Match 49.1%; Score 83; DB 1; Length 153;
 Best Local Similarity 46.7%; Pred. No. 0.00018; 9; Mismatches 9; Indels 0; Gaps 0;
 Matches 14; Conservative 7;

Qy 1 SPKMWQGSGCFGRKMDRISSSGIGCKVLR 30
 Db 121 APRSLRRSSCFCGGRIDRIGAQSGLGCNSFR 150

RESULT 15
 A30162
 brain natriuretic factor precursor - rat
 N;Alternate names: brain natriuretic peptide; cardiac natriuretic factor; iso-atrial n
 N;Contains: brain natriuretic factor BNP 45
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A30162; A35691; A54893; A32918; A32919; A33253; A60735; 157704; A33252
 R;Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 159, 1420-1426, 1989
 A;Title: Cloning and sequence analysis of cDNA encoding a precursor for rat brain natri
 A;Reference number: A30162; MUID:89193742; PMID:2522776
 A;Accession: A30162
 A;Molecule type: mRNA
 A;Residues: 1-121 <KOJ>
 A;Cross-references: GB:M25297; NID:9602483; PIDN:AAA57269.1; PID:g602484
 R;ROY, R.N.; Flynn, T.G.
 Biochem. Biophys. Res. Commun. 171, 416-423, 1990
 A;Title: Organization of the gene for iso-rANP, a rat B-type natriuretic peptide.
 A;Reference number: A35691; MUID:90365739; PMID:2144113
 A;Accession: A35691
 A;Molecule type: DNA
 A;Residues: 1-14, 'V', 16-121 <ROY>
 A;Cross-references: GB:M60731; NID:9204985; PIDN:AAA41456.1; PID:g204986
 A;Note: the authors translated the codon GTT for residue 15 as Ieu
 R;Thuerauf, D.J.; Hanford, D.S.; Glembotski, C.C.
 J. Biol. Chem. 269, 1772-1775, 1994
 A;Title: Regulation of rat brain natriuretic peptide transcription. A potential role f
 A;Reference number: A54893; MUID:94299479; PMID:8027030
 A;Accession: A54893
 A;Molecule type: DNA
 A;Residues: 1-19 <THU>
 A;Cross-references: GB:U02972; NID:9458021; PIDN:AAA21648.1; PID:g458022
 R;Aburaya, M.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 163, 226-232, 1989
 A;Title: Isolation and identification of rat brain natriuretic peptides in cardiac atr
 A;Reference number: A32918; MUID:89374230; PMID:2673236
 A;Accession: A32918
 A;Molecule type: protein
 A;Residues: 27-121 <ABU>
 R;Kambayashi, Y.; Nakao, K.; Itoh, H.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.
 Imura, H.
 Biochem. Biophys. Res. Commun. 163, 233-240, 1989
 A;Title: Isolation and sequence determination of rat cardiac natriuretic peptide.
 A;Reference number: A32919; MUID:89374231; PMID:2528349
 A;Accession: A32919
 A;Molecule type: protein
 A;Residues: 77-121 <KAV>
 R;Flynn, T.G.; Brar, A.; Tremblay, L.; Sarda, I.; Lyons, C.; Jennings, D.B.
 Biochem. Biophys. Res. Commun. 161, 830-837, 1989
 A;Title: Isolation and characterization of iso-rANP, a new natriuretic peptide from ra
 A;Reference number: A33253; MUID:89286593; PMID:2525380
 A;Accession: A33253
 A;Molecule type: protein
 A;Residues: 77-119, 'Q', 121 <FLY>
 R;Nakao, K.; Itoh, H.; Kambayashi, Y.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.
 Hypertension 15, 774-778, 1990
 A;Title: Rat brain natriuretic peptide. Isolation from rat heart and tissue distributi
 A;Reference number: A60735; MUID:90277148; PMID:2351430

A;Accession: A60735
A;Molecule type: protein
A;Residues: 77-121 <NAK>
R;Dagnino, L.; Drouin, J.; Nemer, M.
Mol. Endocrinol. 5, 1292-1300, 1991
A;Title: Differential expression of natriuretic peptide genes in cardiac and extracardiac
A;Reference number: 157704; MUID:92123224; PMID:1837590
A;Accession: 157704
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-121 <RES>
A;Cross-references: GB;M60266; NID:g204983; PIDN:AAA41455.1; PID:g204984
C;Genetics:
A;Introns: 42/3; 117/1
C;Superfamily: natriuretic peptide A precursor
C;Keywords: cardiac muscle; heart
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-121/Product: brain natriuretic factor #status experimental <MAT1>
F;77-121/Product: brain natriuretic factor BNP-45 #status experimental <MAT2>
Query Match 48.5%; Score 82; DB 1; Length 121;
Best Local Similarity 57.1%; Pred. NO. 0.0002; Matches 16; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
Matches 16;
QY 3 KMVQGSGCFGRKMDRISSSGLGCKVLR 30
Db 92 KMAHSSSCFGQKIDRIGAVSRIGCDGLR 119

Search completed: March 29, 2004, 14:43:16
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:35:24 ; Search time 11 Seconds
(without alignments)
151,477 Million cell updates/sec

Title: US-09-902-517-49
Perfect score: 169

Sequence: 1 SPKMQQGCGFGRKMDRISSSGLGCKVLRHH 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42;*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	169	100.0	134 1 ANFB_HUMAN	P16860 homo sapien
2	124	73.4	103 1 ANFB_BOVIN	P13204 bos taurus
3	124	73.4	129 1 ANFB_SHEEP	O46541 ovis aries
4	123	72.8	140 1 ANFB_CANFIA	P16859 canis familiaris
5	122	72.2	131 1 ANFB_PIG	P07634 sus scrofa
6	101	59.8	140 1 ANF_CHICK	P18908 gallus gallus
7	87	51.5	149 1 ANF_CANFA	P07499 canis familiaris
8	87	51.5	150 1 ANF_PIG	P24259 sus scrofa
9	87	51.5	152 1 ANF_BOVIN	P07501 bos taurus
10	87	51.5	152 1 ANF_SHEEP	O46540 ovis aries
11	87	51.5	153 1 ANF_HORSE	P27104 equus caballus
12	87	51.5	153 1 ANF_HUMAN	P01160 homo sapien
13	49.1	153 1 ANF_RABBIT	P07500 oryctolagus cuniculus	
14	82	48.5	121 1 ANFB_RAT	P13205 rattus norvegicus
15	82	48.5	152 1 ANF_MOUSE	P05125 mus musculus
16	82	48.5	152 1 ANF_RAT	P01161 rattus norvegicus
17	81	47.9	128 1 ANF_CAVPO	P27596 cavia porcellus
18	79	46.7	126 1 ANFC_BOVIN	P55206 bos taurus
19	79	46.7	126 1 ANFC_HUMAN	P23582 homo sapiens
20	79	46.7	126 1 ANFC_MOUSE	Q61839 mus musculus
21	79	46.7	126 1 ANFC_PIG	P18104 sus scrofa
22	79	46.7	126 1 ANFC_RAT	P55207 rattus norvegicus
23	79	46.7	126 1 ANFC_SHEEP	P56283 ovis aries
24	78	46.2	39 1 VNOC_OXYSA	P83230 oxyuratus m
25	78	46.2	39 1 VNOC_OXYSA	P83231 oxyuratus s
26	78	46.2	131 1 ANFC_ANGJA	P18145 anguilla japonica
27	77	45.6	36 1 ANFC_ANGJA	P22642 anguilla japonica
28	77	45.6	121 1 ANFB_MOUSE	P40753 mus musculus
29	76	45.0	118 1 ANFD_RANCA	P40756 rana catesbeiana
30	75	44.4	35 1 VNOC_OXYMI	P83229 oxyuratus major
31	75	44.4	35 1 VNOC_OXYSA	P83228 oxyuratus s
32	75	44.4	35 1 VNOC_OXYSC	P23259 scyliorhinus
33	75	44.4	115 1 ANFC_SCYCA	

P55208 triakis scyliorhinus
P18144 anguilla japonica
P20968 rana catesbeiana
P83224 oxyuratus major
P83225 oxyuratus s
P21805 gallus gallus
P09196 rana ridibunda
P18909 rana catesbeiana
P41319 squalus acanthias
P28374 dendroaspis polylepis
Q9pw7 paralichthys

ALIGNMENTS

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scoring table: BLOSUM62

RN	[5]	SEQUENCE OF 27-58 AND 103-134.	ID	ANFB_BOVIN	STANDARD:	PRT:	103 AA.
RP			AC	P13204;			
RX		MEDLINE=90211249; PubMed=2138890;	DT	01-JAN-1990 (Rel. 13, Created)			
RA		Hino J., Tateyaa H., Minamino N., Kangawa K., Matsuo H.;	DT	01-DEC-1992 (Rel. 24, Last sequence update)			
RT		"Isolation and identification of human brain natriuretic peptides in	DT	15-MAR-2004 (Rel. 43, Last annotation update)			
RT		cardiac atrium.;"	DE	Brain natriuretic peptide precursor (BNP) (Aldosterone secretion			
RL		Biochem. Biophys. Res. Commun. 167:693-700(1990).	DE	inhibitory factor) (ASIF).			
RN	[6]		GN	NPPB.			
RP		SEQUENCE OF 103-134.	OS	Bos taurus (Bovine).			
RX		FEBS Lett. 259:341-345(1990).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RA		-!- FUNCTION: Acts as a cardiac hormone with a variety of biological	OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
RA		actions including natriuresis, diuresis, vasorelaxation, and	OC	Bovidae; Bovinae; Bos.			
CC		inhibition of renin and aldosterone secretion. It is thought to	OX	NCBI_TaxID=9913;			
CC		play a key role in cardiovascular homeostasis. Helps restore the	RN	[1]			
CC		body's salt and water balance. Improves heart function.	RP	SEQUENCE.			
CC		-!- SUBCELLULAR LOCATION: Secreted.	RX	MEDLINE=90114187; PubMed=2532709;			
CC		-!- TISSUE SPECIFICITY: Brain and also in atria, but at much lower	RA	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC		levels than ANP.	RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC		-!- PHARMACEUTICAL: Available under the name Nesiritide (Scios). Used	RT	bovine chromaffin cells."			
CC		for the treatment of heart failure.	RL	RT			
CC		-!- SIMILARITY: Belongs to the natriuretic peptide family.	RN	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
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CC			RA	MEDLINE=89136947; PubMed=2537187;			
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CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
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CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
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CC			RA	MEDLINE=89136947; PubMed=2537187;			
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CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
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CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
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CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
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CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
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CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
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CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
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CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
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CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			
CC			CC	RT			
CC			CC	SEQUENCE OF 69-103.			
CC			RA	MEDLINE=89136947; PubMed=2537187;			
CC			RT	Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;			
CC			RT	"Aldosterone secretion inhibitor: a novel neuropeptide in			
CC			RL	bovine chromaffin cells."			

Matches 17; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)

DE (ANP) (Prepronatriodilatin) [Contains: Cardiodilatin-related peptide (CDP)].

DE (CDP)].

GN NPPA.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; NCBI_TaxID=9823;

OX [1]

RN P07499;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)

DE (ANP) (Prepronatriodilatin).

GN NPPA.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=9615;

OX [1]

RN SEQUENCE FROM N.A.

RX MEDLINE-86076957; PubMed=2934062;

RA Okawa S., Imai M., Inuzuka C., Tawaragi Y., Nakazato H., Matsuo H.;

RT "Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from nucleotide sequence of cloned cDNA.";

RL Biochem. Biophys. Res. Commun. 132:892-899(1985).

CC -!- FUNCTION: Atrial natriuretic factor (ANF) is a potent vasoactive substance synthesized in mammalian atria and is thought to play a key role in cardiovascular homeostasis. Has a cGMP-stimulating activity.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- MISCELLANEOUS: A disulfide bond is required for full activity of atriopeptides.

CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

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CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- MISCELLANEOUS: A disulfide bond is required for full activity of atriopeptides.

CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

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DR EMBL; M12045; AAA30828.1; -.

DR A25302; ANDG.

DR InterPro; IPR00663; Natr_peptide.

DR PF00212; ANP; 1.

DR PRINTS; PR00710; NATPEPTIDES.

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.

KW Vasoactive; Signal.

FT SIGNAL 1 23 POTENTIAL.

FT PROPEP 24 120 ATRIAL NATRIURETIC FACTOR.

FT PEPTIDE 122 149 DISULFID

FT PEPTIDE 128 144 SEQUENCE 149 AA; 15819 MW; 9BA3A11C0B7557DB CRC64;

Query Match 51.5%; Score 87; DB 1; Length 149; Best Local Similarity 50.0%; Pred. No. 7.2e-06; Mismatches 6; Indels 0; Gaps 0;

Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 SPKMWQGSGCCFGRKMDRISSSGLGCKVLR 30

DB 119 APRSLRRSSCFCGGRMDRIGAQSGLGCGNSFR 148

Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 SPKMWQGSGCCFGRKMDRISSSGLGCKVLR 30

DB 120 APRSLRRSSCFCGGRMDRIGAQSGLGCGNSFR 149

Query Match 51.5%; Score 87; DB 1; Length 150; Best Local Similarity 50.0%; Pred. No. 7.3e-06; Mismatches 6; Indels 9; Gaps 0;

Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 SPKMWQGSGCCFGRKMDRISSSGLGCKVLR 30

DB 120 APRSLRRSSCFCGGRMDRIGAQSGLGCGNSFR 149

RESULT 8

ID ANF_PIG STANDARD; PRT; 150 AA.

AC P24259; 01-MAR-1992 (Rel. 21, Created)

RESULT 9

ANF_BOVIN

ID	ANF_BOVIN	STANDARD;	PRT;	152 AA.
AC	P07501;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)			
DE	(ANP) (Prepronatriodilatin).			
GN	NPPA.			
OS	Bos taurus (Bovine)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.			
OC	NCBI_TAXID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	Medline=86215205; PubMed=2939830;			
RA	Vlasuk G.P., Miller J., Bencen G.H., Lewicki J.A.,			
RT	"Structure and analysis of the bovine atrial natriuretic peptide precursor gene.;"			
RL	Biochem. Biophys. Res. Commun. 136:396-403 (1986).			
RN	[2]			
RP	SEQUENCE OF 123-150.			
RX	Medline=86173941; PubMed=3007908;			
RA	Ong H., McNicoll N., Lazare C., Seidah N., Chretien M., Cantic M., de Lean A.;			
RT	"Purification and sequence determination of bovine atrial natriuretic factor.;"			
RL	Life Sci. 38:1309-1315(1986).			
CC	-!- FUNCTION: Atrial natriuretic factor (ANF) is a potent vasoactive substance synthesized in mammalian atria and is thought to play a key role in cardiovascular homeostasis. Has a cGMP-stimulating activity.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- MISCELLANEOUS: A disulfide bond is required for full activity of atriopeptins.			
CC	-!- SIMILARITY: Belongs to the natriuretic peptide family.			
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CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- MISCELLANEOUS: A disulfide bond is required for full activity of atriopeptins.			
CC	-!- SIMILARITY: Belongs to the natriuretic peptide family.			
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DR	EMBL; M13145; AAA30375.1; -			
DR	PIR; A90124; AWBO.			
DR	InterPro; IPR002407; At_natriurtcpep.			
DR	InterPro; IPR002408; Br_natriurtcpep.			
DR	InterPro; IPR000663; Natr_peptide.			
DR	Pfam; PF00212; ANP; 1.			
DR	PRINTS; PR00710; NATPEPTIDES.			
DR	DR InterPro; IPR002407; At_natriurtcpep.			
DR	InterPro; IPR000663; Natr_peptide.			
DR	Pfam; PF00212; ANP; 1.			
DR	PRINTS; PR00710; NATPEPTIDES.			
DR	DR ProDom; PD005107; At_natriurtcpep; 1.			
DR	ProDom; PD006651; Br_natriurtcpep; 2.			
DR	SMART; SM00183; NAT_PEP; 1.			
DR	PROSITE; PS00263; NATRIURETIC_PEP; 1.			
KW	Vasoactive; Signal.			
FT	SIGNAL 1 24 POTENTIAL.			
FT	PROPEP 25 121 BY SIMILARITY.			
FT	PEPTIDE 123 150 ATRIAL NATRIURETIC FACTOR.			
FT	DISULFID 129 145 BY SIMILARITY.			
SQ	SEQUENCE 152 AA; 16368 MW; 5FA82C6E1325E7C6 CRC64;			
Query Match	51.5%; Score 87; DB 1; Length 152;			
Best Local Similarity	50.0%; Pred. No. 7.4e-06;			
Matches	15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;			
QY	1 SPKMKVQGSGCFGRKMDRISSSGLGCKVLR 30			
DB	120 APRSLRRSSCFGGRMDRIGAQSGLGCGNSFR 149			
RESULT 11				
ANF_HORSE	STANDARD;	PRT;	153 AA.	
ID	ANF_HORSE			
AC	P27104;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)			

DE (ANP) (Prepronatriotriiodilatin).
 GN NPPA.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=Adamiticus; TISSUE=Heart atrium;
 RA Maegert H.J., Richter R., Schmaedding G., Forssmann W.-G.;
 RL Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
 CC -I- FUNCTION: Atrial natriuretic factor (ANF) is a potent vasoactive
 CC substance synthesized in mammalian atria and is thought to play a
 CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
 CC activity.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- MISCELLANEOUS: A disulfide bond is required for full activity of
 CC atriopeptins.
 CC -I- SIMILARITY: Belongs to the natriuretic peptide family.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X58563; CAA41443.1; -.
 DR Interpro; IPR000663; Natr_peptide.
 DR PIR; S14873; S14873.
 DR PRINTS; PR00710; NAT_PEP; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Vasoactive; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT PROPER 26 122
 FT PEPTIDE 124 151 ATRIAL NATRIURETIC FACTOR.
 FT DISULFID 130 146 BY SIMILARITY.
 SQ SEQUENCE 153 AA; 16825 MW; AFC19471DF564BD7 CRC64;
 RL
 RN 51.5%; Score 87; DB 1; Length 153;
 Best Local Similarity 50.0%; Pred. No. 7.4e-06;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 DB
 OY 1 SPKMWQGSGCFGRKMDRISSSSGIGCKVLR 30
 121 APRSLRRSSCFFGMRIGAQSGLGONSFR 150
 RESULT 12
 ANF_HUMAN STANDARD; PRT; 153 AA.
 ID ANF_HUMAN STANDARD; PRT; 153 AA.
 AC P01160; Q13766;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
 (ANP) (prepronatriotriiodilatin) [Contains: Cardiodilatin-related peptide
 (CDP)].
 DE NPPA OR PND.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE OF 1-151 FROM N.A.
 RX MEDLINE=84219799; PubMed=6203042;
 RA Okawa S., Imai M., Ueno A., Tanaka S., Noguchi T., Nakazato H.,
 RA Kangawa K., Fukuda A., Matsuo H.;
 RT "Cloning and sequence analysis of cDNA encoding a precursor for human
 atrial natriuretic polypeptide.";
 RL Nature 309: 724-726 (1984).
 RN [2]
 SEQUENCE OF 1-151 FROM N.A.
 RP MEDLINE=84295577; PubMed=6547996;
 RX Nakayama K., Onkubo H., Hirose T., Inayama S., Nakaniishi S.;
 RA "mRNA sequence for human cardiotriiodilatin-atrial natriuretic factor
 precursor and regulation of precursor mRNA in rat atria.";
 RT Nature 310:699-701 (1984).
 RN [3]
 SEQUENCE OF 1-151 FROM N.A.
 RP RX
 RA Nemer M., Chamberland M., Sirois D., Argentin S., Drouin J.,
 RA Dixon R.A.F., Zivin R.A., Condra J.H.;
 RT "Gene structure of human cardiac hormone precursor,
 RT pronatriotriiodilatin.";
 RL Nature 312:654-656 (1984).
 RN [4]
 SEQUENCE OF 1-151 FROM N.A.
 RP RX
 RA Greenberg B.D., Bencen G.H., Seilhamer J.J., Lewicki J.A.,
 RA Fiddes J.C.;
 "Nucleotide sequence of the gene encoding human atrial natriuretic
 factor precursor.";
 RT Nature 312:656-658 (1984).
 RN [5]
 SEQUENCE OF 1-151 FROM N.A.
 RP RX
 RA Seidman C.E., Bloch K.D., Klein K.A., Smith J.A., Seidman J.G.;
 RT factor genes";
 RA Seidman C.E., Bloch K.D., Zisfein J., Smit J., Haber E., Homcy C.,
 RT "Nucleotide sequences of the human and mouse atrial natriuretic
 factor genes";
 RA Duby A.D., Choi E., Graham R.M.; Seidman J.G.;
 RT Science 226:1206-1209 (1984).
 RN [6]
 SEQUENCE OF 1-151 FROM N.A.
 RP RX
 RA Seidman C.E., Bloch K.D., Zisfein J., Smit J., Haber E., Homcy C.,
 RT "Molecular studies of the atrial natriuretic factor gene.";
 RA RT
 RL Hypertension 7:131-134 (1985).
 RN [7]
 SEQUENCE OF 1-151 FROM N.A.
 RP RX
 RA Errington H.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RL
 RN [8]
 SEQUENCE FROM N.A.
 RP RC
 TISSUE=Prostate;
 MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL
 RN [9]
 SEQUENCE OF 1-18-153 FROM N.A.
 RP MEDLINE=85038509; PubMed=6238331;
 RX Zivin R.A., Condra J.H., Dixon R.A.F., Seidah N.G., Chretien M.,
 RA Nemer M., Chamberland M., Drouin J.,
 RT "Molecular cloning and characterization of DNA sequences encoding rat
 and human atrial natriuretic factors.";

RL	PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).	FT VARIANT 32 32 V -> M (in dbSNP:5063).
RN	[110]	FT /FTId=VAR 014579.
RP	SEQUENCE OF 1-75 FROM N.A.	FT MISSING (IN isoform 2).
RX	MEDLINE=85096983; PubMed=6097248;	FT /FTId=VAR 000594.
RA	Maki M., Parmentier M., Inagami T.;	FT E -> D (IN REF. 6).
RT	"Cloning of genomic DNA for human atrial natriuretic factor.";	FT
RL	Biochem. Biophys. Res. Commun. 125:797-802(1984).	SEQUENCE 153 AA; 16708 MW; B38F03AA066A73EC CRC64;
RN	[111]	SEQUENCE OF 124-151.
RA	Kangawa K., Matsuo H.;	RP MEDLINE=84128019; PubMed=6230082;
RT	"Purification and complete amino acid sequence of alpha-human atrial natriuretic polypeptide (alpha-HANP).";	RT
RX	Fairbrother W.J., McDowell R.S., Cunningham B.C.;	RT Biochem. Biophys. Res. Commun. 118:131-139(1984).
RA	"Solution conformation of an atrial natriuretic peptide variant selective for the type A receptor.";	RN
RL	Biochemistry 33:8897-8904(1994).	STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR.
RX	MEDLINE=94318633; PubMed=8043577;	RP
RA	Fairbrother W.J., McDowell R.S., Cunningham B.C.;	CC
RT	"Solution conformation of an atrial natriuretic peptide variant selective for the type A receptor.";	CC
CC	Biochemistry 33:8897-8904(1994).	CC
CC	-!- SUBCELLULAR LOCATION: Secreted.	CC
CC	-!- POLYMORPHISM: There are two different prepronatriodilatin alleles.	CC
CC	One codes for 2 Arg residues at the C-terminus that are cleaved to form the mature peptide, while the other ends in a termination codon immediately after the last codon of the mature peptide.	CC
CC	-!- SIMILARITY: Belongs to the natriuretic peptide family.	CC
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CC	--	CC
DR	EMBL; X01470; CAA25699.1; -.	DR
DR	EMBL; X02558; CAA25699.1; JOINED.	DR
DR	EMBL; K02043; AAB59379.1; -.	DR
DR	EMBL; X01471; CAA25700.1; ALT_SEQ.	DR
DR	EMBL; K02044; AAS1730.1; -.	DR
DR	EMBL; AL02115; CAA15955.1; -.	DR
DR	EMBL; BC005893; AAH05893.1; -.	DR
DR	EMBL; M30262; AAA35669.1; -.	DR
DR	EMBL; M54947; AAA35529.1; -.	DR
DR	EMBL; M54951; AAA35529.1; JOINED.	DR
DR	EMBL; K02399; AAA35528.1; -.	DR
DR	PIR; A22693; AWU.	DR
DR	PDB; 1ANP; 07-APR-95.	DR
DR	Genew; HGNC: 7939; NPPA.	DR
DR	MIM; 108780; -.	DR
DR	GO; GO:0005576; C:extracellular; NAS.	DR
DR	GO; GO:0005179; F:hormone activity; NAS.	DR
DR	GO; GO:0008217; P:regulation of blood pressure; IDA.	DR
DR	InterPro; IPR02407; At_natriurtcpep.	DR
DR	InterPro; IPR002408; Br_natriurtcpep.	DR
DR	InterPro; IPR002408; Br_natriurtcpep.	DR
DR	InterPro; IPR00653; Natr_peptide.	DR
DR	Pfam; PF00212; ANP; 1.	DR
DR	PRINTS; PR00710; NATPEPTIDES.	DR
DR	ProDom; PD005107; At_natriurtcpep; 1.	DR
DR	ProDom; PD006651; Br_natriurtcpep; 2.	DR
DR	SMART; SM00183; NAT_PEP; 1.	DR
DR	SMART; SM00183; NAT_PEP; 1.	DR
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.	DR
KW	Vasoactive; Signal; Polymorphism; 3D-structure.	FT
FT	SIGNAL 1 25 POTENTIAL.	FT
FT	PROPE 26 122 ATRIAL Natriuretic Factor.	FT
FT	PEPTIDE 124 151 ATRIAL Natriuretic Factor.	FT
FT	PROPER 56 122 ATRIAL Natriuretic Factor.	FT
FT	DISULFID 130 146 ATRIAL Natriuretic Factor.	FT
SQ	SEQUENCE 153 AA; 16843 MW; 8214A56D073D3236 CRC64;	SQ
Query Match	49.1%; Score 83; DB 1; Length 153;	Score 87; DB 1; Length 153;
Query	1 SPKMQVGSGCFGRKMDRISSSGLGCKVLR 30	Best Local Similarity 50.0%; Pred. No. 7.4e-06; Mismatches 9; Indels 0; Gaps 0;
Db	121 APRSLRRSSCFFGRMDRIGAQSGLGCNSFR 150	Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy	1 SPKAVQGSGCFFGRKMDRISSSSGLGCKVLR 30	RT "Occurrence of a novel cardiac natriuretic peptide in rats.";
Db	121 APRSLRRSSCFCGGRIDRIGAQSGLGCNSFR 150	RL Biochem. Biophys. Res. Commun. 161:732-739 (1989).
RESULT 14		CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
ANFB_RAT	STANDARD; PRT; 121 AA.	CC actions including natriuresis, diuresis, vasorelaxation, and
ID		CC inhibition of renin and aldosterone secretion. It is thought to
ANFB_RAT		CC play a key role in cardiovascular homeostasis. Helps restore the
AC	P13205;	CC body's salt and water balance. Improves heart function.
DT	01-JAN-1990 (Rel. 13, Created)	CC -!- SUBCELLULAR LOCATION: Secreted.
DT	01-FEB-1991 (Rel. 17, Last sequence update)	CC -!- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
DT	15-MAR-2004 (Rel. 43, Last annotation update)	CC levels than ANP.
DE	Brain natriuretic peptide precursor (BNP) (5 kDa cardiac natriuretic	CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
DE	peptide) (ISO-ANP).	CC
GN	Rattus norvegicus (Rat).	CC
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CC
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	CC
OX	NCBI_TaxID=10116;	CC
RN	[1]	CC
RP	SEQUENCE FROM N.A.	CC
RX	MEDLINE=89193742; PubMed=2522776;	DR EMBL; M25297; AAA57269.1; -.
RA	Kojima M., Minamino N., Kangawa K., Matsuo H.;	DR EMBL; M60731; AAA41456.1; -.
RT	"Cloning and sequence analysis of cDNA encoding a precursor for rat	DR EMBL; M60266; AAA41455.1; -.
RT	brain natriuretic peptide.";	DR PIR; A30162; A30162.
RL	Biochem. Biophys. Res. Commun. 159:1420-1426(1989).	DR InterPro; IPR002408; Br_natriurtcpep.
RN	[2]	DR PIAM; PF00212; ANP; 1.
RP	SEQUENCE FROM N.A.	DR PRINTS; PR00710; NATPEPTIDES.
RX	MEDLINE=90365739; PubMed=2144113;	DR PRODom; PD006651; Br_natriurtcpep; 1.
RA	Roy R.N., Flynn T.G.;	DR SMART; SM00183; NAT _{PEP} ; 1.
RT	"Organization of the gene for iso-ANP, a rat B-type natriuretic	DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
RL	peptide.";	DR KW Vasoactive; Signal.
RN	Biochem. Biophys. Res. Commun. 171:416-423 (1990).	FT SIGNAL; 1 26
RP	SEQUENCE FROM N.A.	FT PEPTIDE 1 121 GAMMA-BRAIN NATRIURETIC PEPTIDE.
RX	MEDLINE=92123224; PubMed=1837590;	FT PEPTIDE 77 121 BRAIN NATRIURETIC PEPTIDE (5 kDa CARDIAC
RA	Dagino L., Drouin J., Nemer M.;	FT DISULFID 99 115
RT	"Differential expression of natriuretic peptide genes in cardiac and	FT CONFLICT 15 15 L -> V (IN REF. 2).
RT	extracardiac tissues.";	FT CONFLICT 120 120 L -> Q (IN REF. 6).
RL	Mol. Endocrinol. 5:1292-1300(1991).	FT SEQUENCE 121 AA; 13656 MW; B5D4151ED18C7294 CRC64;
RN	[4]	CC
RP	SEQUENCE OF 27-121.	Query Match
RX	MEDLINE=89374230; PubMed=2673236;	Best Local Similarity 48.5%; Score 82; DB 1; Length 121;
RA	Abuyara M., Hino J., Minamino N., Kangawa K., Matsuo H.;	Matches 16; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
RT	"Isolation and identification of rat brain natriuretic peptides in	Qy 3 KPKAVQGSGCFFGRKMDRISSSSGLGCKVLR 30
RL	cardiac atrium.";	Db 92 KMAHSSSCFGQKIDRIGAVSRLGCDGLR 119
RN	Biomed. Biophys. Res. Commun. 163:226-232(1989).	CC
RP	[5]	RESULT 15
RC	SEQUENCE OF 77-121.	ANF_MOUSE
RX	TISSUE=Heart;	ID ANF_MOUSE STANDARD; PRT; 152 AA.
RA	MEDLINE=89374231; PubMed=2528349;	AC P05125;
RA	Kambayashi Y., Nakao K., Itoh H., Hosoda K., Saito Y., Yamada T.,	DT 13-AUG-1987 (Rel. 05, Created)
RA	Mukoyama M., Arai H., Shirakami G., Suga S.-I., Ogawa Y.,	DT 10-OCT-2003 (Rel. 42, Last annotation update)
RA	Jougasaki M., Minamino N., Kangawa K., Matsuo H., Inouye K., Imura H.;	DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
RT	"Isolation and sequence determination of rat cardiac natriuretic	DE (ANP) (Prepronatriotriiodilatin).
RT	peptide.";	DE (ANP) (Prepronatriotriiodilatin).
RL	Biochem. Biophys. Res. Commun. 163:233-240(1989).	GN NPPA OR PND.
RN	[6]	OS Mus musculus (Mouse).
RP	SEQUENCE OF 77-121.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RX	MEDLINE=89286593; PubMed=2525380;	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RA	Flynn T.G., Brar A., Tremblay L., Sarda I., Lyons C., Jennings D.B.;	NCBI_TaxID=10090;
RT	"Isolation and characterization of iso-ANP, a new natriuretic	RN [1]
RT	peptide from rat atria.";	RP SEQUENCE FROM N.A.
RL	Biochem. Biophys. Res. Commun. 161:830-837(1989).	RX MEDLINE=85065766; PubMed=6542248;
RN	[7]	RA Seidman C.E., Bloch K.D., Klein K.A., Smith J.A., Seidman J.G.;
RP	SEQUENCE OF 99-115.	RT "Nucleotide sequences of the human and mouse atrial natriuretic
RX	MEDLINE=89286579; PubMed=2525379;	RT factor genes.";
RA	Itoh H., Nakao K., Kambayashi Y., Hosoda K., Saito Y., Yamada T.,	RT Science 226:1205-1209(1984).
RA	Mukoyama M., Arai H., Shirakami G., Suga S.-I., Yoshida T., Inouye K.,	RA
RA	Imura H.;	CC -!- FUNCTION: Atrial natriuretic factor (ANF) is a potent vasoactive
		CC substance synthesized in mammalian atria and is thought to play a

CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: A disulfide bond is required for full activity of
 CC atriopeptins.
 CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
 CC
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 DR EMBL; K02781; AAA37235.1; -.
 DR PIR; A29370; AWMS.
 DR MGD; MGI; 97367; Nppa.
 DR InterPro; IPR002407; At_natriureticpep.
 DR InterPro; IPR000663; Natri_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR PRODOM; PD005107; At_natriureticpep; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Vasooactive; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 124
 FT PEPTIDE 126 149 AURICULIN A (BY SIMILARITY).
 FT PEPTIDE 126 150 AURICULIN B (BY SIMILARITY).
 FT PEPTIDE 127 149 ATROPEPTIN I (BY SIMILARITY).
 FT PEPTIDE 127 147 ATROPEPTIN II (BY SIMILARITY).
 FT DISULFID 129 145 BY SIMILARITY.
 SQ SEQUENCE 152 AA; 16645 MW; FC8CC43EAAFC227 CRC64;

Query Match 48.5%; Score 82; DB 1; Length 152;
 Best Local Similarity 48.3%; Pred. No. 4.1e-05;
 Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY	2 PRMVQGSGCFGRKMDRISSSGLGCKVLR 30
Db	121 PRSLRRSSCFGRIDRIGAQSGLGCNSFR 149

Search completed: March 29, 2004, 14:41:50
 Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:36:39 ; Search time 39 Seconds

(without alignments)
258.887 Million cell updates/sec

Title: US-09-902-517-49
Perfect score: 169
Sequence: 1 SPKMWQGSGCFGRKMDRISSSGLGCKVLRRH 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archaeap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	118	69.8	112	6	Q9GLK5	Q9glk5 felis silve
2	118	69.8	132	6	Q9GLK4	Q9glk4 felis silve
3	96	56.8	126	13	Q8AYRS	Q8ayrs oryzae lat
4	92	54.4	146	13	Q7T2I7	Q7t2i7 oncorhynchus
5	92	54.4	152	13	Q9YQJ1	Q9yqj1 salmo salar
6	91	53.8	138	13	Q805E8	Q805e8 oreochromis
7	91	53.8	146	13	Q7T1Q2	Q7t1q2 oryzae lat
8	90	53.3	130	13	Q805D5	Q805d5 fugu rubrip
9	88	52.1	162	5	Q7YZU5	Q7yzu5 eptatretus
10	87	51.5	152	6	Q9TQW1	Q9tqw1 balaenopter
11	87	51.5	153	6	Q9GLD0	Q9gl0 felis silve
12	87	51.5	155	6	Q29130	Q29130 tupaia bela
13	86	50.9	181	13	Q90Y12	Q90y12 crotalus du
14	86	50.9	181	13	Q90Y11	Q90y11 crotalus du
15	83	49.1	140	13	Q805E9	Q805e9 oreochromis
16	82	48.5	120	13	Q805D3	Q805d3 fugu rubrip

Query	Match	Length	DB	ID	Description				
1	SPKMWQGSGCFGRKMDRISSSGLGCKVLRRH	32	17	82	48.5	121	13	Q80017	Q80017 oryzae lat
18	82	48.5	133	13	Q805D7	Q805d7 fugu rubrip			
19	82	48.5	152	11	Q8VRH2	Q8vrh2 notomyale			
20	81	47.9	139	13	P79799	P79799 micrurus co			
21	79	46.7	33	11	Q9QZ96	Q9qz96 cavia porce			
22	79	46.7	126	13	Q805D6	Q805d6 fugu rubrip			
23	79	46.7	131	13	Q8AYR6	Q8ayr6 oryzae lat			
24	79	46.7	131	13	Q8AXR3	Q8axr3 oncorynchu			
25	79	46.7	131	13	Q8AXR2	Q8axr2 oncorynchu			
26	79	46.7	131	13	Q805E7	Q805e7 oreochromis			
27	79	46.7	147	11	Q8VHG9	Q8vhg9 notomyale			
28	78	46.2	139	13	Q805D8	Q805d8 fugu rubrip			
29	77	45.6	121	11	Q91V40	Q91v40 mus spicile			
30	77	45.6	121	11	Q55086	Q55086 mus musculus			
31	77	45.6	144	13	Q805E6	Q805e6 fundulus he			
32	77	45.6	150	13	Q9PSV2	Q9psv2 anguilla ja			
33	76	45.0	140	13	Q9PSV1	Q9psv1 anguilla ja			
34	76	45.0	221	13	Q7T1M4	Q7t1m4 bothrops ja			
35	76	45.0	263	13	Q9PT52	Q9pt52 agkistrodon			
36	76	45.0	265	13	Q8QG91	Q8qg91 bothrops in			
37	75	44.4	111	6	Q8HXV7	Q8hxv7 pan troglod			
38	75	44.4	111	6	Q8HXV6	Q8hxv6 gorilla gor			
39	75	44.4	111	6	Q8HXV5	Q8hxv5 ponga pygma			
40	75	44.4	111	6	Q8HXV4	Q8hxv4 macaca sp			
41	75	44.4	111	6	Q8HXV3	Q8hxv3 saginus oe			
42	75	44.4	136	13	Q98UJ7	Q98ui7 triakis scy			
43	75	44.4	265	13	Q9PW56	Q9pw56 bothrops ja			
44	72	42.6	150	13	Q90X61	Q90x61 bufo marinus			
45	71.5	42.3	147	13	Q9DGK8	Q9dgk8 xenopus lae			

ALIGNMENTS

RESULT	1	Q9GLK5	ID	Q9GLK5	PRELIMINARY;	PRT;	112 AA.
AC	Q9GLK5;	DT	01-MAR-2001	(TREMBLrel. 16, Created)			
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)					
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)					
DE	Brain	natriuretic peptide (Fragment).					
DS	Felis	silvestris catus (Cat).					
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis; NCBITaxID=9685;						
RN	[1]	SEQUENCE FROM N.A.					
RP	RA	Liu Z.L., Wiedmeyer C.E., Solter P.F., Sisson D.D.;					
RT	"Cat brain natriuretic peptide gene.";						
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AF251261; AAC13660.1; -;						
DR	GO; GO:0005576; C:extracellular; IEA.						
DR	GO; GO:005179; F:hormone activity; IEA.						
DR	InterPro; IPR002408; Br_natriuretpe.						
DR	InterPro; IPR000653; Natr_peptide.						
DR	PFam; PF00212; ANP; 1.						
DR	PRINTS; PRO0710; NATPEPTIDES.						
DR	PRODom; PD006651; Br_natriuretpep; 1.						
DR	SMART; SM00183; NAT_PEP; 1.						
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.						
FT	NON_TER	1	1				
FT	NON_TER	112	112				
SQ	SEQUENCE	112 AA;	12083	MM;	580224FL12984FFB2	CRC64;	

Query	Match	Length	DB	ID	Description				
1	SPKMWQGSGCFGRKMDRISSSGLGCKVLRRH	32	17	82	48.5	121	13	Q80017	Q80017 oryzae lat
18	82	48.5	133	13	Q805D7	Q805d7 fugu rubrip			
19	82	48.5	152	11	Q8VRH2	Q8vrh2 notomyale			
20	81	47.9	139	13	P79799	P79799 micrurus co			
21	79	46.7	33	11	Q9QZ96	Q9qz96 cavia porce			
22	79	46.7	126	13	Q805D6	Q805d6 fugu rubrip			
23	79	46.7	131	13	Q8AYR6	Q8ayr6 oryzae lat			
24	79	46.7	131	13	Q8AXR3	Q8axr3 oncorynchu			
25	79	46.7	131	13	Q8AXR2	Q8axr2 oncorynchu			
26	79	46.7	131	13	Q805E7	Q805e7 oreochromis			
27	79	46.7	147	11	Q8VHG9	Q8vhg9 notomyale			
28	78	46.2	139	13	Q805D8	Q805d8 fugu rubrip			
29	77	45.6	121	11	Q91V40	Q91v40 mus spicile			
30	77	45.6	121	11	Q55086	Q55086 mus musculus			
31	77	45.6	144	13	Q805E6	Q805e6 fundulus he			
32	77	45.6	150	13	Q9PSV2	Q9psv2 anguilla ja			
33	76	45.0	140	13	Q9PSV1	Q9psv1 anguilla ja			
34	76	45.0	221	13	Q7T1M4	Q7t1m4 bothrops ja			
35	76	45.0	263	13	Q9PT52	Q9pt52 agkistrodon			
36	76	45.0	265	13	Q8QG91	Q8qg91 bothrops in			
37	75	44.4	111	6	Q8HXV7	Q8hxv7 pan troglod			
38	75	44.4	111	6	Q8HXV6	Q8hxv6 gorilla gor			
39	75	44.4	111	6	Q8HXV5	Q8hxv5 ponga pygma			
40	75	44.4	111	6	Q8HXV4	Q8hxv4 macaca sp			
41	75	44.4	111	6	Q8HXV3	Q8hxv3 saginus oe			
42	75	44.4	136	13	Q98UJ7	Q98ui7 triakis scy			
43	75	44.4	265	13	Q9PW56	Q9pw56 bothrops ja			

RESULT 2

ID Q9GLK4 PRELIMINARY; PRT; 132 AA.

AC Q9GLK4; 01-MAR-2001 (TREMBrel. 16, Created)

DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)

DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)

DE Brain natriuretic peptide.

GN BNP.

OS Felis silvestris catus (Cat).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Felidae; Felis.

OX NCBI_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart atrium;

RA Liu Z.L., Wiedmeyer C.E., Solter P.F., Sisson D.D.;

RT "Cat mRNA for brain natriuretic peptide (BNP)." ; Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RL [2]

RN RP SEQUENCE FROM N.A.

RA Liu Z.L.;

RT "Felis catus brain natriuretic peptide (BNP) gene." ; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF253495; AAG13661.1; -

DR EMBL; AF425738; AAL24812.1; -

DR GO; GO:005576; C:extracellular; IEA.

DR GO; GO:005179; F:hormone activity; IEA.

DR InterPro; IPR002408; Br_natriurtcpep.

DR Pfam; PF00212; ANP; 1.

DR PRINTS; PR00710; NATPEPTIDES.

DR ProDom; P006651; Br_natriurtcpep; 1.

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

SQ SEQUENCE

132 AA; 1434 MW; D069B5F76A6C3510 CRC64;

Query Match 69.8%; Score 118; DB 6; Length 132;

Best Local Similarity 68.8%; Pred. No. 1.4e-09;

Matches 22; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 101 SSKMMRDRSRCFGRRDRIGSISGGCINLRRH 132

RESULT 4

ID Q7T217 PRELIMINARY; PRT; 146 AA.

AC Q7T217; 01-OCT-2003 (TREMBrel. 25, Created)

DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DE Atrial natriuretic peptide.

GN Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RA Inoue K., Russel M.J., Olson K.R., Takei Y.; (Oncorhynchus mykiss): "C-type natriuretic peptide of rainbow trout (Oncorhynchus mykiss): primary structure and vasorelaxant activities." ; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AB076603; BAC77769.1; -

DR SEQUENCE 146 AA; 16043 MW; FED2CE3C79121BDO CRC64;

Query Match 54.4%; Score 92; DB 13; Length 146;

Best Local Similarity 70.8%; Pred. No. 1.1e-05;

Matches 17; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 122 SGCFGRKMDRISSSSGIGCKVLR 31

RESULT 5

ID Q9YQJ1 PRELIMINARY; PRT; 152 AA.

AC Q9YQJ1; 01-MAY-1999 (TREMBrel. 10, Created)

DT 01-MAY-1999 (TREMBrel. 10, Last sequence update)

DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)

DE Cardiac hormone (Cardiac peptide precursor).

OS Salmo salar (Atlantic salmon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

OC Baloniformes; Adrianichthyidae; Oryziinae; Oryzias.

OC Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzias.

OX NCBI_TaxID=8090;

RN [1]

RP SEQUENCE FROM N.A.

RA Inoue K., Takei Y.;

RT "C-type natriuretic peptide of medaka (Oryzias latipes)." ; Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB081456; BAC15761.1; -

DR GO; GO:005576; C:extracellular; IEA.

DR GO; GO:005179; F:hormone activity; IEA.

DR InterPro; IPR000663; Natr_peptide.

DR Pfam; PF00212; ANP; 1.

DR PRINTS; PR00710; NATPEPTIDES.

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SMART; SM00183; NAT_PEP; 1.

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Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SMART; SM00183; NAT_PEP; 1.

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DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

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Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

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DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SMART; SM00183; NAT_PEP; 1.

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DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

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DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DR Qy 4 MVQGSGCFGRKMDRISSSSGIGC 26

Db 104 MVAGGGCFGGMKMDRIGSISGLGC 126

DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPITIDE; 1.

DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECBOFF92 CRC64;

DR SQ

Query Match 56.8%; Score 96; DB 13; Length 126;

Best Local Similarity 78.3%; Pred. No. 2.4e-06;

Matches 18;

DR	InterPro; IPR000663; Natr_peptide.
DR	Pfam; PF00212; ANP; 1.
DR	PRINTS; PR00710; NATPEPTIDES.
DR	SMART; SM00183; NAT_PEP; 1.
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW	Signal.
FT	CHAIN 124 152 AA; 16740 MW; CARDIAC HORMONE.
SQ	SEQUENCE 152 AA; 16740 MW; E1D3E38A159CFBAA CRC64;
QY	8 SGCFGRKMDRISSSGLGCKVLR 31
Db	128 SGCFGRMDRIGTSSGLGCKSPKR 151
RESULT 6	
Q805E8	PRELIMINARY; PRT; 138 AA.
AC	Q805E8;
DT	01-JUN-2003 (TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	B-type natriuretic peptide.
GN	BNP.
OS	Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Oreochromis.
OX	NCBI_TaxID=8127;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	
RA	Inoue K., Takei Y.;
RT	"Natriuretic Peptides of Tilapia"; Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AB087284; BAC55025.1; -.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005179; F:hormone activity; IEA.
DR	InterPro; IPR000663; Natr_peptide.
DR	Pfam; PF00212; ANP; 1.
DR	PRINTS; PR00710; NATPEPTIDES.
DR	SMART; SM00183; NAT_PEP; 1.
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
SQ	SEQUENCE 138 AA; 15189 MW; 5A023AB1F4F452FA CRC64;
QY	53.8%; Score 91; DB 13; Length 138; Best Local Similarity 59.3%; Pred. No. 1.4e-05; Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Db	6 QGSGCFGRKMDRISSSGLGCKVLRH 32
QY	6 QGSGCFGRKMDRISSSGLGCKVLRH 32
Db	107 RSSGCFGRMDRIGSNSLIGCNTVGRY 133
RESULT 7	
Q7T1Q2	PRELIMINARY; PRT; 146 AA.
AC	Q7T1Q2;
DT	01-OCT-2003 (TREMBLrel. 25, Created)
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	B-type natriuretic peptide.
GN	BNP.
OS	Oryzias latipes (Japanese ricefish). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Beloniiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC	NCBI_TaxID=8090;
OX	
QY	54.4%; Score 92; DB 13; Length 152; Best Local Similarity 70.8%; Pred. No. 1.1e-05; Matches 17; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Db	8 SGCFGRKMDRISSSGLGCKVLR 31
QY	53.8%; Score 91; DB 13; Length 146; Best Local Similarity 59.3%; Pred. No. 1.5e-05; Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Db	6 QGSGCFGRKMDRIGSNSLIGCNTVGRY 143
RESULT 8	
Q805D5	PRELIMINARY; PRT; 130 AA.
AC	Q805D5;
DT	01-JUN-2003 (TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	C-type natriuretic peptide-2.
GN	CNP-2.
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes; Osteidae; Tetraodontidae; Tetraodontidae; Takifugu.
OX	NCBI_TaxID=31033;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	
RA	Inoue K., Takei Y.;
RT	"Six natriuretic peptide genes in the pufferfish genome. "; Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AB089936; BAC57072.1; -.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005179; F:hormone activity; IEA.
DR	InterPro; IPR000663; Natr_peptide.
DR	Pfam; PF00212; ANP; 1.
DR	PRINTS; PR00710; NATPEPTIDES.
DR	SMART; SM00183; NAT_PEP; 1.
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
SQ	SEQUENCE 130 AA; 13792 MW; 41BE1FCC1AS7E4C CRC64;
QY	53.3%; Score 90; DB 13; Length 130; Best Local Similarity 73.9%; Pred. No. 1.9e-05; Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Db	4 MVQGSGCFGRKMDRISSSGLG 26
QY	4 MVQGSGCFGRKMDRISSSGLG 26
Db	108 MVGGRGCFGMKIDRIGSISGLG 130
RESULT 9	
Q7Y2U5	PRELIMINARY; PRT; 162 AA.
AC	Q7Y2U5;
DT	01-OCT-2003 (TREMBLrel. 25, Created)
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Natriuretic peptide.
GN	Eptatretus burgeri (Inshore hagfish).
OS	Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes; Myxinidae; Eptatretinae; Eptatretus.
OC	Myxiniformes; Eptatretinae; Eptatretus.
OC	NCBI_TaxID=7764;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Kawakoshi A., Hyodo S., Takei Y.;

RT "Hagfish natriuretic peptide precursor mRNA of *Eptatretus burgeri*.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; AB087732; BAC78816.1; -.
 PT CHAIN 94 161 natriuretic peptide.
 SQ 162 AA; 18220 MW; F4E866403FLA48F7 CRC64;

Query Match 52.1%; Score 88; DB 5; Length 162;
 Best Local Similarity 69.6%; Pred. No. 4.7e-05; 4; Mismatches 3; Indels 0; Gaps 0;
 Matches 16; Conservative 3; Gaps 0;

QY 9 GCFGRKMDRISSSSGLGCKVLR 31
 Db 135 GCFGVKMDRIGASTGLGCGARR 157

RESULT 10

Q9TQW1 PRELIMINARY; PRT; 152 AA.

ID Q9TQW1
 AC Q9TQW1;
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Atrial natriuretic peptide precursor.
 OS Balaenoptera physalus (Finback whale) (Common rorqual).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OC NCBI_TaxID=9770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Taskinen T.H.; Vuolehto O.J.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; AJ006755; CAB65023.1; -.
 DR EMBL; AJ006785; CAB64785.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTEIDE; 1.
 KW Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 150 ATRIAL NATRIURETIC PEPTIDE.
 SQ SEQUENCE 152 AA; 16454 MW; 513133C664038FF6 CRC64;

Query Match 51.5%; Score 87; DB 6; Length 152;
 Best Local Similarity 50.0%; Pred. No. 6.2e-05;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 Gaps 0;

QY 1 SPKMQVQGSGCFGRKMDRISSSSGLGCKVLR 30
 Db 120 APRSLRRSSCFCGRMDRIGAQSGLGCGNSFR 149

RESULT 11

Q9GLD0 PRELIMINARY; PRT; 153 AA.

ID Q9GLD0
 AC Q9GLD0;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Atrial natriuretic peptide.
 OS *Felis silvestris catus* (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Biondo A.W.; Liu Z.L.; Solter P.F.; Sisson D.D.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; AF298813; AAG23837.1; -.

RESULT 12

Q29130 PRELIMINARY; PRT; 155 AA.

ID Q29130
 AC Q29130;
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Cardiodilatin, atrial natriuretic peptide.
 OS *Tupaia belangeri* (Northern tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaidae; Tupaia.
 OC NCBI_TaxID=37347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Schneidemann S.; Maegert H.J.; Forssmann W.G.;
 RT "nucleotide sequence of the cDNA for *Tupaia belangeri* cardiodilatin /
 atrial natriuretic peptide.";
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Pardigol A.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; Z70294; CAA94310.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR002408; Br_natriurtcpep.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR proDom; PD006551; Br_natriurtcpep; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTEIDE; 1.
 SQ SEQUENCE 155 AA; 16860 MW; 22BF05A3748DAB68 CRC64;

Query Match 51.5%; Score 87; DB 6; Length 155;
 Best Local Similarity 50.0%; Pred. No. 6.3e-05;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 SPKMQVQGSGCFGRKMDRISSSSGLGCKVLR 30
 Db 123 APRSLRRSSCFCGRMDRIGAQSGLGCGNSFR 152

RESULT 13

Q90Y12 PRELIMINARY; PRT; 181 AA.

ID Q90Y12
 AC Q90Y12;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Bradykinin potentiating peptide and C-type natriuretic peptide isoform 1.
 DE Crotalus durissus terrificus (South American rattlesnake).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Q805E9	PRELIMINARY;	PRT;	140 AA.
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;	ID	Q805E9		
OC	Viperidae; Crotalinae; Crotalus.	AC	Q805E9;		
OX	NCBI_TAXID=8732;	DT	01-JUN-2003 (TREMBLrel: 24, Created)		
RN	[1] SEQUENCE FROM N.A.	DT	01-JUN-2003 (TREMBLrel: 24, Last sequence update)		
RC	TISSUE=Venom gland;	DT	01-OCT-2003 (TREMBLrel: 25, Last annotation update)		
RA	Hayashi M.A.F., Radis-Baptista G., Barbosa S.R., Yamane T.,	DE	Atrial natriuretic peptide.		
RA	Camargo A.C.M.; "Crotalus durissus terrificus bradykinin potentiating peptide precursor.",	GN			
RT	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.	OS	Oreochromis mossambicus (Mozambique tilapia) (<i>Tilapia mossambica</i>).		
RL	EMBL; AF308593; AAL09426.1; -.	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DR	GO; GO:0005576; C:extracellular; IEA.	OC	Actinopterygii; Neopterygii; Teleostei; Neoteleostei;		
DR	GO; GO:0005179; F:hormone activity; IEA.	OC	Acanthopterygii; Percomorpha; Perciformes; Labroidei;		
DR	InterPro; IPR00663; Natr_peptide.	OC	Cichlidae; Oreochromis.		
DR	Pfam; PF00212; ANP; 1.	NCBI_TAXID=8127;			
DR	PRINTS; PRO0710; NATPEPTIDES.	RN			
DR	SMART; SM00183; NAT_PEP; 1.	RP			
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.	RC			
SQ	SEQUENCE 181 AA; 18560 MW; 7B5ADC5B9372D07F CRC64;	RT			
Query Match	50.9%; Score 86; DB 13; Length 181;	TISSUE=Heart;			
Best Local Similarity	75.0%; Pred. No. 0.0001; Length 181;	Inoue K., Takei Y.;			
Matches	15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	"Natriuretic Peptides of Tilapia";			
QY	7 GSGCFGKMDRISSSSGLGC 26	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
Db	162 GNGCFGKLDRIGSMSGLGC 181	EMBL; AB087283; BAC55024.1; -.			
RESULT 14		GO; GO:0005576; C:extracellular; IEA.			
Q90Y11	PRELIMINARY; PRT; 181 AA.	GO; GO:0005179; F:hormone activity; IEA.			
ID		InterPro; IPR02408; Br_natriurtcpep.			
AC	Q90Y11; 01-DEC-2001 (TREMBrel: 19, Created)	InterPro; IPR00663; Natr_peptide.			
DT	01-DEC-2001 (TREMBrel: 19, Last sequence update)	Pfam; PF00212; ANP; 1.			
DT	01-JUN-2003 (TREMBrel: 24, Last annotation update)	PRINTS; PRO0710; NATPEPTIDES.			
DE	Bradykinin potentiating peptide and C-type natriuretic peptide isoform 2.	PRODOM; PD006651; Br_natriurtcpep; 1.			
OS	Crotalus durissus terrificus (South American rattlesnake).	SMART; SM00183; NAT_PEP; 1.			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;	SEQUENCE 140 AA; 15577 MW; 5F2D214FA560DB0F CRC64;			
NCBI_TAXID=8732;					
RN	[1] SEQUENCE FROM N.A.	Query Match	49.1%; Score 83; DB 13; Length 140;		
RC	TISSUE=Venom gland;	Best Local Similarity	73.7%; Pred. No. 0.00022; Length 140;		
RA	Hayashi M.A.F., Radis-Baptista G., Barbosa S.R., Yamane T.,	Matches	14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;		
RA	Camargo A.C.M.; "Crotalus durissus terrificus bradykinin-potentiating peptide and C-type natriuretic peptide precursor isoform2.",	QY	8 GSGCFGKMDRISSSSGLGC 26		
RT	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.	Db	117 GNGCFGKLDRIGSMSGLGC 135		
RL	EMBL; AF308594; AAL09427.1; -.	Search completed: March 29, 2004, 14:42:42			
DR	GO; GO:0005576; C:extracellular; IEA.	Job time : 40 secs			
DR	GO; GO:0005179; F:hormone activity; IEA.				
DR	InterPro; IPR00663; Natr_peptide.				
DR	Pfam; PF00212; ANP; 1.				
DR	PRINTS; PRO0710; NATPEPTIDES.				
DR	SMART; SM00183; NAT_PEP; 1.				
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.				
SQ	SEQUENCE 181 AA; 18507 MW; 9B2E95D38AA5FF27 CRC64;				
Query Match	50.9%; Score 86; DB 13; Length 181;				
Best Local Similarity	75.0%; Pred. No. 0.0001; Length 181;				
Matches	15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;				
QY	7 GSGCFGKMDRISSSSGLGC 26				
Db	162 GNGCFGKLDRIGSMSGLGC 181				

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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:41:55 ; Search time 14 Seconds
(without alignments)
41.857 Million cell updates/sec

Title: US-09-902-517-49
Perfect score: 169
Sequence: 1 SPKMQGSGCFGRKMDRISSSGLGCKVLRRH 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 152794 seqs, 18312476 residues

Total number of hits satisfying chosen parameters: 152794

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	100.0	32	6	US-10-775-204-1802
2	169	100.0	134	6	US-10-775-204-1277
3	169	100.0	641	6	US-10-775-204-1634
4	169	100.0	719	6	US-10-775-204-1275
5	87	51.5	32	6	US-10-775-204-2203
6	87	51.5	153	6	US-10-796-307-725
7	78	46.2	28	6	US-10-775-204-2207
8	78	46.2	31	6	US-10-681-389-22
9	50.5	29.9	657	1	PCT-US04-05092-28
10	49	29.0	874	6	US-10-487-092-18
11	47.5	28.1	1307	6	US-10-796-307-608
12	46.5	27.5	147	6	US-10-767-701-46988
13	45	26.6	116	6	US-10-767-701-33741
14	45	26.6	182	6	US-10-767-701-32774
15	44.5	26.3	378	5	US-09-979-167-123
16	44	26.0	219	6	US-10-100-683-8839
17	44	26.0	220	6	US-10-799-747-135
18	44	26.0	241	6	US-10-767-701-35710
19	44	26.0	682	6	US-10-649-400-4
20	43.5	25.7	209	1	PCT-US04-05654-1900
21	43	25.4	173	6	US-10-767-701-45583
22	43	25.4	331	6	US-10-767-701-46510
23	43	25.4	996	1	PCT-US04-05654-512
24	42	24.9	145	6	US-10-767-701-44616
25	42	24.9	281	6	US-10-767-701-44746
26	42	24.9	312	6	US-10-767-701-45391

ALIGNMENTS

RESULT 1
US-10-775-204-1802
; Sequence 1802, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; Sequence 2203, AP
; Sequence 725, APP
; Sequence 2207, AP
; Sequence 22, APP
; Sequence 28, APP
; Sequence 18, APP
; Sequence 608, APP
; Sequence 46988, A
; Sequence 33741, A
; Sequence 32774, A
; Sequence 123, APP
; Sequence 8839, APP
; Sequence 135, APP
; Sequence 35710, A
; Sequence 4, APP1
; Sequence 1900, APP
; Sequence 45583, A
; Sequence 46510, A
; Sequence 512, APP
; Sequence 44616, A
; Sequence 44746, A
; Sequence 45391, A

Query Match 100.0%; Score 169; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPKMQGSGCFGRKMDRISSSGLGCKVLRRH 32
Db 1 SPKMQGSGCFGRKMDRISSSGLGCKVLRRH 32

RESULT 2

US-10-775-204-1277

; Sequence 1277, Application US/10775204

; GENERAL INFORMATION:

; APPLICANT: Rosen, Craig A.

; APPLICANT: Haseltine, William A.

; APPLICANT: Balance, David J.

; APPLICANT: Turner, Andrew J.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF564

CURRENT APPLICATION NUMBER: US/10/775, 204

CURRENT FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/341, 811

PRIOR FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/360, 000

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/378, 950

PRIOR FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/398, 008

PRIOR FILING DATE: 2002-07-24

PRIOR APPLICATION NUMBER: 60/411, 355

PRIOR FILING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: 60/414, 984

PRIOR FILING DATE: 2002-10-02

PRIOR APPLICATION NUMBER: 60/417, 611

PRIOR FILING DATE: 2002-10-11

PRIOR APPLICATION NUMBER: 60/420, 246

PRIOR FILING DATE: 2002-10-23

PRIOR APPLICATION NUMBER: 60/423, 623

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: 60/351, 360

PRIOR FILING DATE: 2002-01-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2222

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1277

LENGTH: 134

TYPE: PRT

ORGANISM: Homo sapiens

US-10-775-204-1634

RESULT 4

Query Match 100.0%; Score 169; DB 6; Length 641;

Best Local Similarity 100.0%; Pred. No. 4.7e-17; Mismatches 0; Indels 0; Gaps 0;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPKMWQGSGCFGRKMDRISSSGLGCKVLRRH 32

Db 25 SPKMWQGSGCFGRKMDRISSSGLGCKVLRRH 56

RESULT 3

US-10-775-204-1634

; Sequence 1634, Application US/10775204

; GENERAL INFORMATION:

; APPLICANT: Rosen, Craig A.

; APPLICANT: Haseltine, William A.

; APPLICANT: Balance, David J.

; APPLICANT: Turner, Andrew J.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF564

CURRENT APPLICATION NUMBER: US/10/775, 204

PRIOR APPLICATION NUMBER: 60/341, 811

PRIOR FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/360, 000

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/378, 950

PRIOR FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/398, 008

PRIOR APPLICATION NUMBER: 60/411, 355

PRIOR FILING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: 60/414, 984

PRIOR FILING DATE: 2002-10-02

PRIOR APPLICATION NUMBER: 60/417, 611

PRIOR FILING DATE: 2002-10-11

PRIOR APPLICATION NUMBER: 60/420, 246

PRIOR FILING DATE: 2002-10-23

PRIOR APPLICATION NUMBER: 60/423, 623

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: 60/351, 360

PRIOR FILING DATE: 2002-01-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2222

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1275

LENGTH: 719

TYPE: PRT

ORGANISM: Homo sapiens

US-10-775-204-1275

Query Match 100.0%; Score 169; DB 6; Length 719;

Best Local Similarity 100.0%; Pred. No. 5.3e-17; Mismatches 0; Indels 0; Gaps 0;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPKMQVGGCFGRKMDRISSSGLGCKVLRH 32
 Db 103 SPKMQVGGCFGRKMDRISSSGLGCKVLRH 134

RESULT 5
 US-10-775-204-2203
 ; Sequence 2203, Application US/10775204
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Haseltine, William A.
 ; APPLICANT: Balance, David J.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF564
 ; CURRENT APPLICATION NUMBER: US/10/775, 204
 ; CURRENT FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/341, 811
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 60/360, 000
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: 60/378, 950
 ; PRIOR FILING DATE: 2002-05-10
 ; PRIOR APPLICATION NUMBER: 60/398, 008
 ; PRIOR FILING DATE: 2002-07-24
 ; PRIOR APPLICATION NUMBER: 60/411, 355
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: 60/414, 984
 ; PRIOR FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: 60/417, 611
 ; PRIOR FILING DATE: 2002-10-11
 ; PRIOR APPLICATION NUMBER: 60/420, 246
 ; PRIOR FILING DATE: 2002-10-23
 ; PRIOR APPLICATION NUMBER: 60/423, 623
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: 60/351, 360
 ; PRIOR FILING DATE: 2002-01-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2222
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 2203
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-775-204-2203

Query Match 51.5%; Score 87; DB 6; Length 32;
 Best Local Similarity 50.0%; Pred. No. 1.8e-06; Mismatches 15; Conservatve 6; Indels 9; Gaps 0; Gaps 0;
 Matches 15; Conservatve 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 SPKMQVGGCFGRKMDRISSSGLGCKVLR 30
 Db 2 APRSLRRSSCFCGGRMDRIGAQSGGCGNSFR 31

RESULT 6
 US-10-796-307-725
 ; Sequence 725, Application US/10796307
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01509
 ; CURRENT APPLICATION NUMBER: US/10/796, 307
 ; CURRENT FILING DATE: 2004-03-10
 ; NUMBER OF SEQ ID NOS: 44201
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 725
 ; LENGTH: 153
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-775-204-2207

Query Match 51.5%; Score 87; DB 6; Length 32;
 Best Local Similarity 50.0%; Pred. No. 1.8e-06; Mismatches 15; Conservatve 6; Indels 9; Gaps 0; Gaps 0;
 Matches 15; Conservatve 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 SPKMQVGGCFGRKMDRISSSGLGCKVLR 30
 Db 2 APRSLRRSSCFCGGRMDRIGAQSGGCGNSFR 31

RESULT 7
 US-10-775-204-2207
 ; Sequence 2207, Application US/10775204
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Haseltine, William A.
 ; APPLICANT: Balance, David J.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF564
 ; CURRENT APPLICATION NUMBER: US/10/775, 204
 ; CURRENT FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/341, 811
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 60/360, 000
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: 60/378, 950
 ; PRIOR FILING DATE: 2002-05-10
 ; PRIOR APPLICATION NUMBER: 60/398, 008
 ; PRIOR FILING DATE: 2002-07-24
 ; PRIOR APPLICATION NUMBER: 60/411, 355
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: 60/414, 984
 ; PRIOR FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: 60/417, 611
 ; PRIOR FILING DATE: 2002-10-11
 ; PRIOR APPLICATION NUMBER: 60/420, 246
 ; PRIOR FILING DATE: 2002-10-23
 ; PRIOR APPLICATION NUMBER: 60/423, 623
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: 60/351, 360
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2222
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 2207
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-775-204-2207

Query Match 46.2%; Score 78; DB 6; Length 28;
 Best Local Similarity 46.2%; Pred. No. 3.3e-05; Mismatches 14; Conservatve 2; Indels 7; Gaps 0; Gaps 0;
 Matches 14; Conservatve 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 SPKMQVGGCFGRKMDRISSSGLGCKVLR 30
 Db 2 APRSLRRSSCFCGGRMDRIGAQSGGCGNSFR 31

RESULT 8
 US-10-681-389-22
 ; Sequence 22, Application US/10681389
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenten, John H
 ; APPLICANT: Tramontano, Alfonso
 ; APPLICANT: Pilon, April L
 ; APPLICANT: Lohnas, Gerald L
 ; APPLICANT: Roberts, Steven F
 ; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
 ; FILE REFERENCE: U.S. Patent Application No. 09\026,276
 ; CURRENT APPLICATION NUMBER: US/10/681,389
 ; CURRENT FILING DATE: 2003-10-07
 ; PRIOR APPLICATION NUMBER: US/09/964, 201A

PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-681-389-22

Query Match 46.2%; Score 78; DB 6; Length 31;
Best Local Similarity 60.9%; Pred. No. 3.7e-05; Mismatches 7; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 8 SGCFGRKMDRISSSGLGCKVLR 30
Db 8 SSCFGGRMDRIGAQSGLGNCNSFR 30

RESULT 9
PCT-US04-05092-28
; Sequence 28, Application PC/TUS0405092
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; RAMKUMAR, Jayalaxmi;
; APPLICANT: MARQUIS, Joseph P.; SWARNAKAR, Anita;
; APPLICANT: CHAWLA, Narinder K.; TRAN, Uyen K.;
; APPLICANT: BECHA, Shanya ; LEE, Soo Yeun;
; APPLICANT: HAFALIA, April J.A.; RICHARDSON, Thomas;
; APPLICANT: KHARE, Reena; JIANG, Xin;
; APPLICANT: JACKSON, Alan; YANG, Junming;
; APPLICANT: GORVAD, Ami
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PF-1643 PCT
; CURRENT APPLICATION NUMBER: PCT/US04/05092
; CURRENT FILING DATE: 2004-02-20
; PRIORITY NUMBER: US 60/449,059
; PRIORITY FILING DATE: 2003-02-20
; PRIORITY APPLICATION NUMBER: US 60/456,932
; PRIORITY FILING DATE: 2003-03-19
; PRIORITY APPLICATION NUMBER: US 60/458,844
; PRIORITY FILING DATE: 2003-03-28
; PRIORITY APPLICATION NUMBER: US 60/461,678
; PRIORITY FILING DATE: 2003-04-09
; PRIORITY FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: 7517520CD1.
; PCT-US04-05092-28

Query Match 29.9%; Score 50.5; DB 1; Length 657;
Best Local Similarity 44.8%; Pred. No. 12; Mismatches 5; Indels 6; Gaps 5;
Matches 13; Conservative 5; Mismatches 6; Indels 5; Gaps 2;
QY 1 SPKMVQGSGGGFGRKMDRISSSGLGCKVLR 29
Db 566 SPEVISGEG-YGRKADWVS---LGCTVV 589

RESULT 10
US-10-487-092-18
; Sequence 18, Application US/10487092
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; YUE, Henry
; APPLICANT: LU, Dylung Aina M.; SWARNAKAR, Anita;
; APPLICANT: TANG, Y. Tom; GRIFFIN, Jennifer A.;
; APPLICANT: EMERLING, Brooke M.; FORSYTHE, Ian J.;
; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;

RESULT 11
US-10-796-307-608
; Sequence 608, Application US/10796307
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001509
; CURRENT APPLICATION NUMBER: US/10/796,307
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 44201
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 608
; LENGTH: 1307
; TYPE: PRT

; ORGANISM: Homo sapiens
; US-10-796-307-608

Query Match 28.1%; Score 47.5; DB 6; Length 1307;
Best Local Similarity 38.7%; Pred. No. 69;
Matches 12; Conservative 4; Mismatches 6; Indels 9; Gaps 1;
Qy 10 CFGRRKMDRISSS-----GLGCKVLRR 31
Db 5 CSGRLIERSSSSPRASCWSRGCGCHLNRR 35

RESULT 12
US-10-767-701-46988

; Sequence 46988, Application US/10767701
; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 46988

; LENGTH: 147

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE: OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_322.pep

US-10-767-701-46988

Query Match 27.5%; Score 46.5; DB 6; Length 147;

Best Local Similarity 40.6%; Pred. No. 8.7;

Matches 13; Conservative 4; Mismatches 12; Indels 3; Gaps 1;

Qy 3 KMYQQGSGCFGRKM--DRISSSGLGCKVLRR 31
Db 16 KGLGSSISGRKLAWSRPPSSARAACRSTRR 47

RESULT 13
US-10-767-701-33741

; Sequence 33741, Application US/10767701
; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 33741

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE: OTHER INFORMATION: Clone ID: SORBI-28MAY03-C36286_1.pep

US-10-767-701-33741

Query Match 26.6%; Score 45; DB 6; Length 116;
Best Local Similarity 42.1%; Pred. No. 11;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 13 RKMDRISSSSGLGCKVLRR 31
Db 4 KWMERTSITGPGSCTIRK 22

RESULT 14



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 118013

TO: Janet Epps-Ford
Location: rem/2c05/2c18
Art Unit: 1635
Monday, March 29, 2004

Case Serial Number: 09/902517

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Epps-Ford,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib

118013

From: Epps-Ford, Janet
Sent: Friday, March 26, 2004 4:52 PM
To: STIC-Biotech/ChemLib
Subject: Protein sequence Search

Please search SEQ ID NO: 49 of application 09/902,517 in all pending and commercial amino acid databases.

Thanks.

Janet L. Epps-Ford, Ph.D.

Art Unit 1635

Mailbox: Remsen 2C18

Office: Remsen 2C05

Phone: 571-272-0757

Fax: 571-273-0757

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